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Run
                                                                                      OM protein - nucleic search, using frame_plus_p2n model
                                                  9n:
December 20, 2002, 12:02:33 ; Search time 190.526 Seconds (without alignments) 118.199 Million cell updates/sec
                                                                                                                                                       GenCore version Copyright (c) 1993 - 2002
                                                                                                                                                         5.1.3
Compugen Ltd.
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Scoring table: Perfect score: Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 US-10-008-355-25 54 TGGNSGSPVF 10 0.5 7.0 7.0

Searched: 2185239 seqs, 1125999159 residues

Minimum DB Maximum DB seq length: 0 length: 2000000000 Total number of hits satisfying chosen parameters:

4370478

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USETQ_spool/US10008355/runat_17122002_112336_14573/app_query.fasta_1...
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER=US10008355_@CGN_1_1_0_@trunat_17122002_112336_14573 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPPXT=0.5 -FGAPOP=6 -FGAPEXT=7

Database N_Geneseq_101002:*

// SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985_DAT: *
// SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986_DAT: *
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// SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994_DAT: *
// SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000_DAT: * /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.

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SUMMARIES

Result No.

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colon car	n secreted		Pseudomonas sp Typ	Human secreted pro	DNA encoding C. al	rgillus oryz	man brain	#9954	prosta	neoaing p	an rung ar	e	rium vene	n pro	Bacillus lichenifo	Bacillus lichenifo	OVE	Human ORFX polynuc	n immune/	מ			ovarian	~	de sequen	_	_	<u> 1</u>	m.	coccus fae	idney injury	E faecalis EF110 q	nterococcu	E faecalis EF110 o	Futerococcis faeca		Tuermitura	capnyrococcus	. epidermidis	orpnyromonas g	re	rotease from S.	ococcus au		Description

ALIGNMENTS

AAV75063; AAV75063 standard; DNA; 1019 BP.

RESULT 1 AAV75063

Staphylococcus aureus contig SEQ ID #752. 16-MAR-1999 (first entry)

FH XXX Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus

Key Location/Qualifiers

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AAQ27
                                                                                                                                                    RESULT
                                                                                                                                                                                                                                             US-10-008-355-25 (1-10) x AAV75063 (1-1019)
                                                                                                                                                                                                                                                                                  Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, which is the story of the shock.
                                                                                                                                                                                                                                                                                                               Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                           skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences computer readable medium.
                     Protease from S. Aureus
                                                    11-FEB-1993
                                                                                    AAQ27988;
                                                                                                                AAQ27988 standard; DNA; 1558
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1019 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1646-1647; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stored on computer readable medium
anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide(s) and proteins derived stored on computer readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-1997;
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                                                                                                                                                                                                   ThrGlyGlyAsnSerGlySerProValPhe 10
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                                                    (first entry)
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                             159 G; 240
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Matches:
Conservative:
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AAQ27987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from Staphylococcus aureus strains. The DNA sequences were is by PCR using the primer sequences given in AAQ27960-86. The p specifically cleaves the peptide bond at the C-terminus of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel protease prepd. using Bacillus or Saccharomyces host - capable of cleaving peptide bond at carboxyl terminus of glu acid residues in polypeptide(s)
                             sig_peptide
                                                                                                                 Staphylococcus
                                                                                                                                                  Protease; PCR;
                                                                                                                                                                                                                  11-FEB-1993
                                                                                                                                                                                                                                                                                  AAQ27987 standard; DNA; 1586
                                                                                                                                                                                                                                                                                                                                                      1050 ACTGGTGGTAATTCAGGTTCACCTGTATTT 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 15-16; 25pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         he sequences given in AAQ27987-88 encode proteases which were isolated irom Staphylococcus aureus strains. The DNA sequences were isolated
                                                                                                                                                                                                                                                                                                                                                                      1 ThrGlyGlyAsnSerGlySerProValPhe 10
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                                                                                                                                                                                 S. Aureus ATCC12600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residue in
                                                                                                                 aureus
                                                                                                                                                amplify; Staphylococcus;
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                             /*tag= a
352..555
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/*tag= b
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                                                                                Location/Qualifiers
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RESULT 4
AAL43635
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                       DB:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                        1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Staphylococcus aureus strains. The DNA sequences were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide band at the C-terminus of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protease prepd. using Bacillus or Saccharomyces capable of cleaving peptide bond at carboxyl terminus acid residues in polypeptide(s)
                                                                                                                                                                                           Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                  05-SEP-2002
                                                                                                                                                                                                                                                                                             AAL43635 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1586 BP; 590 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ27987-88 encode proteases which were isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 13~15; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-304938/37.
P-PSDB; AAR26842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP04211370-A
                     08-NOV-2000; 2000US-246827P
                                                                                     WO200238742-A2
                                                                                                                                                               Porphyromonas
                                                                                                                                                                                                                             Porphyromonas
                                                                                                                                                                                                                                                                        AAL43635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamic acid residue in polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1992.
(UYGE-) UNIV GEORGIA RES FOUND INC.
                                         08-NOV-2001; 2001WO-US46782
                                                                16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                             No : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                           1 ThrGlyGlyAsnSerGlySerProValPhe 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scores:
                                                                                                                                                                                                                                                                                                                                       ACTGGTGGTAACTCAGGTTCACCAGTATTT 1077
                                                                                                                                                                                                                                                                                                                                                                                 (1-10)
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                            gingivalis.
                                                                                                                                                                                                                           gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence
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                                                                                                                               Location/Qualifiers
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/product= "Porphyromonas gingivalis
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Matches:
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidglepptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present DNA sequence encodes the Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
Nucleic acids encoding useful for vaccinating
                                        WPI; 2001-316495/33.
P-PSDB; AAG81635.
                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SR1
                                                                                                                                                                                                                                                                                                                                                    03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                               AAH52485;
                                                                                                                                                                                                                                                                                                                                                                                                         AAH52485 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2139 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the invention.
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                                                                                                                                                                    09-NOV-2000;
                                                                                                                                                                                               17-MAY-2001.
                                                                                                                                                                                                                           WO200134809-A2
                                                                                                                                                                                                                                                    Staphylococcus epidermidis.
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                                                                                                                                          09-NOV-1999;
                                                                                                                                                                                                                                                                                 vaccination;
                                                                                                              (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThrGlyGlyAsnSerGlySerProValPhe 10
                                                                                                                                                                                                                                                                                                                        epidermidis
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                                                                                                                                                                    2000WO-US30782
                                                                                                                                                                                                                                                                               endocarditis; ds.
                                                                                                                                                                                                                                                                                                                        open reading
                                                                                                                                        99US-0164258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.73
54.00
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                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x AAL43635
polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis
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                                                                                                                                                                                                                                                                                                                                                                                                           849
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                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                        frame nucleotide sequence SEQ
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                                                                                                                                                                                                                                                                                            strain; infection; diagnosis;
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Conservative:
Mismatches:
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RESULT 6
ABN91429
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polypucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
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Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                           Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                           13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                              30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial;
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                                                                                P-PSDB; ABP38884.
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97US-064964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermidis ORF nucleic acid sequence SEQ ID NO:892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene;
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s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria
                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                               Nucleic acids encoding useful for vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-316495/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200134809-A2
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                                                                                                        AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimmerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2000; 2000WO-US30782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
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                                                                                                                                                                                                                                                            8,
                                                                                                                                                                                                                                                      Page 1307-1308; 2188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0164258
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                                                                                                                                                                                                                                                                                                               polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
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ds.
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Indels:
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RESULT 8
AAL17622
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                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
               The invention relates to human breast cancer expressed polynucleotides (AALO/544-AAL26789) and methods of assessing whether a patient is affilted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human breast cancer expressed polynucleotide 10079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL17622 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                        Claim
                                                                                                                                                                                                                                            WPI; 2001-451856/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2000; 2000US-0176077
14-MAR-2000; 2000US-0189167
24-MAR-2000; 2000US-0192099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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  detecting, diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2001; 2001WO-US00798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001
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                                                                                                                                                                                              New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO . .
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                                                                                                                                                   Page 1799; 3695pp; English.
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2000US-0205230.
2000US-0211315.
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                                                                                                                                                                                                                                                                                     Wang Y,
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100.00%
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monitoring,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВÞ
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Conservative:
Mismatches:
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Gaps:
  characterising
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RESULT 9
AAL00017
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Best Local Similarity:
Query Match:
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                               14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                        28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                 04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
                                                                                                                    14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                            14-AUG-
14-AUG-
                                                                                                                                                       07-JUL-2000
                                                                                                                                                                                                  19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.
                                                                                                                                                11-JUL-2000
                                                                                                                                                                                                                                                                                                         02-AUG-2001
                                                                                                                                                                                                                                                                                                                          WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                                    Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                     Human reproductive system related antigen cDNA SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAL00017;
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                                                                                                                                                                                                                                                                                                                                                            cancer; gene therapy;
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                                                                         2000US-0214886.

2000US-0215135.

2000US-0216647.

2000US-0216880.

2000US-0217487.

2000US-0217496.

2000US-0217496.

2000US-022963.

2000US-022964.

2000US-0224518.

2000US-0224518.

2000US-0225213.

2000US-0225214.
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2000US-0180628
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                                                                                                                                                                                                  2000US-0205515
2000US-0209467
                                                                                                                                                                                                                                     2000US-0186350
2000US-0189874
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44.00
90.00%
70.00%
81.48%
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Matches:
Conservative:
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RESULT 10
AAX20213
ID AAX20
XX
AC AAX20
XX
DT 20-AP
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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01.DEC-2000
05.DEC-2000
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                                                                              AAX20213
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 423
  20-APR-1999
                                        AAX20213;
                                                                                                                                                                                                                                                                                                                                                                       No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
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                                                                                                                                                          300
                                                                                                                                                    2001-465570/50.
DB; AAM94047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                            standard; DNA; 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention provides the protein and coding sequences of uman reproductive system related antigens. These can be ention and treatment of reproductive system disorders, ancer. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0249208
2000US-0249211
2000US-0249211
2000US-0249213
2000US-0249214
2000US-0249214
2000US-0249216
2000US-0249216
2000US-0249217
2000US-0249245
2000US-0249245
2000US-0249264
2000US-0249264
2000US-0249264
2000US-0249297
2000US-0249297
2000US-0251989
2000US-02519856
2000US-0251856
2000US-0251868
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0251989
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                             C;
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Matches:
Conservative:
Mismatches:
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22-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
28-SEP-2000
29-SEP-2000
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23-SEP-2000
24-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
28-NOV-2000
29-SEP-2000
20-OCT-2000
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2000US-0226868
2000US-0227093
2000US-0229343
2000US-0229343
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2000US-0229509
2000US-0229509
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2000US-0229509
2000US-0231243
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2000US-0231241
2000US-0231241
2000US-0231241
2000US-02332081
2000US-0233063
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2000US-0233063
2000US-0233063
2000US-02346476
2000US-02464776
2000US-0246611
2000US-0246528
2000US-0246611
2000US-0246611

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RESULT 11
ABN98198
ID ABN98
XX
AC ABN98
XY
DT 05-AU
XX
Enter
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SS Enter
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Query
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 212-213; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9850554-A2
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                                                                                                                                                                                                    05-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 758 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines {\sf P}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-070095/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; attenuation;
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                         Enterococcus faecalis
                                                                           gene;
                                                                                                  Enterococcus;
                                                                                                                                                                                                                                                   ABN98198
                                                                                                                                                                                                                                                                                                 ABN98198 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY00223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                    575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match:
                                                                                                                                                   faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                 ACCGGCGGTCAATCTGGTTCACCAATCTAT 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scores:
                                                                           ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH,
                                                                                                                                                   EF110
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              faecalis
                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0066009.
97US-0044031.
97US-0046655.
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                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 A;
                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x AAX20213 (1-758)
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                                                                                                                                              fragment
                                                                                               gastrointestinal disease; diagnosis; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
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                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                    14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi
                                                                                                                                                                                                                                                    AAX20212 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 197-198; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes and polypeptides from Enterococcus faecalis, useful vaccines for preventing, treating or attenuating an infection a member of the Enterococcus genus in an animal, particularly faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-425450/45.
P-PSDB; ABP43442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1998;
                                                                            04-MAY-1998;
                                                                                                                                                          detection; attenuation; antigenic; ss
                                                                                                                                                                      Enterococcus faecalis;
                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                 AAX20212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-1998;
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                                                                                                                                      Enterococcus
                                                                                                                                                                                                             20-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002
                (HUMA-) HUMAN GENOME SCI INC
                                                                                                12-NOV-1998
                                                                                                                                                                                                                                                                                            575
                                                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                           GH,
                                                                                                                                                                                                                                                                                                                                                                                                                   Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bailey C,
                                                                                                                                                                                                                                                                                                                                  (1-10)
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                       faecalis.
                                                                                                                                                                                        faecalis gene EF110
                                    97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0071035
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                                                                                                                                                                                                                                                                                                                                                                                                                                     248 A;
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44.00
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                                                                                                                                                                                                                                                    DNA;
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                                                                                                                                                                     infection; vaccine;
                                                                                                                                                                                                                                                    888
                                                                                                                                                                                                                                                                                                                                                                                                                                      143
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                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                   (1-758)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      160 G;
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Matches:
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                                                                                                                                                                     immune response; diagnosis;
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Bailey C,

Choi GH,

Hromockyj

A

Kunsch CA;

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Query
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Pred. No.:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                             [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 212; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                            04-MAY-1998;
                                                                                                                                                                                 04-MAY-1998;
                                                                                                                                                                                                                              US2002045737-A1
                                                                                                                                                                                                                                                                                                                                    05-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 888
                                        New genes and polypeptides from Enterococcus faecalis, useful as vaccines for preventing, treating or attenuating an infection ca
                                                                                                                                                                                                                                                     Enterococcus faecalis
                                                                                                                                                                                                                                                                                     Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic;
                                                                                                                                                                                                                                                                                                                                                          ABN98197
                                                                             P-PSDB;
                                                                                                                                                                                                        18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                               ABN98197 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match:
                                                                                                                                                                                                                                                                                                                                                                                                                             703
                                                                                                                                                                                                                                                                                                             faecalis
                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence represents a gene isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrGlyGlyAsnSerGlySerProValPhe 10
                                                                                        2002-425450/45.
                                                                                                                                                                                                                                                                                                                                                                                                                            ACCGGCGGTCAATCTGGTTCACCAATCTAT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-070095/06.
                                                                             ABP43441
                       for preventing, tree of the Enterococcus
                                                                                                              Bailey C,
                                                                                                                                                                                                                                                                                                             EF110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                            98US-0071035
                                                                                                                                                                                 98US-0071035
                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 A;
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                                                                                                            Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                888
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                               genus
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Indels:
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Conservative:
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                                                                                                              Kunsch
                                an
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                                animal,
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                               E.
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Claim 1;

Page

255pp; English

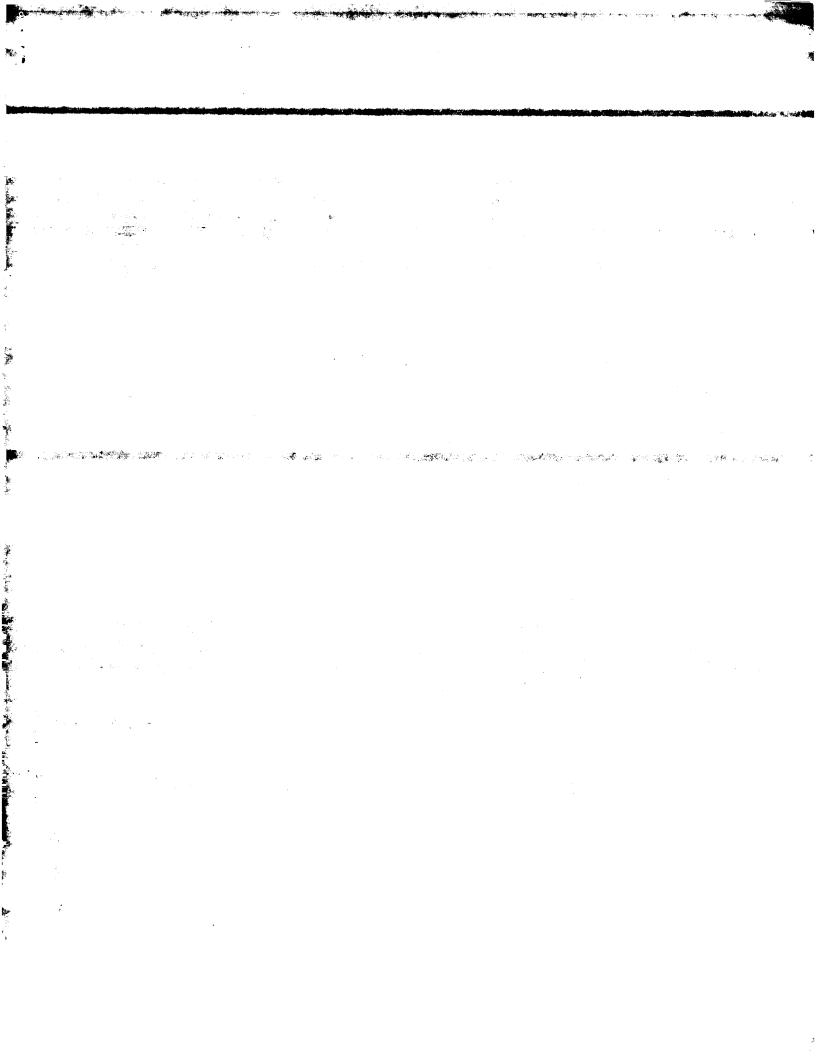
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
            (KIM) cDNA clone. KIM proteins can be administered therapeutically by expressing KIM encoding polynucleotides, to promote growth and/or survival of damaged tissue (e.g. renal tissue), since the KIM proteins are upregulated in injured or regenerating (especially renal) tissues.
                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis
                                                                                                                               Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour; ds.
                                                                                           Claim
                                                                                                                                                                       P-PSDB; AAW86338
                                                                                                                                                                                                               Cate
                                                                                                                                                                                                                                                                 23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                         22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1999
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                                                                                                                                                                                                                                      (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                   26-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection. The present sequence is a coding sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۳
fusion proteins,
                                                                present sequence represents a kidney injury associated molecule
                                                                                                                    regeneration,
                                                                                                                                                                                     1999-045312/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlyGlyAsnSerGlySerProValPhe
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                                                                                       Page 186-188; 213pp; English.
                                                                                                                                                                                                               Hession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated molecule
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97US-0047490.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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 conjugates,
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                                                                                                                                                                                                               Sanicola-Nadel
                                                                                                                                                                                                                                                                                                                                                                                     "kidney injury
                                                                                                                   to treat renal conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-888)
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 antibodies and
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RESULT 15
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06-MAY-1997;
16-MAY-1997;
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                                                                                     New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/prophylaxis of conditions associated with disfunction/disregulation of KIM genes or proteins, especially renal diseases or impairments of rena
Claim 1; Page 1248-1251; 2084pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1999
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                                                                                                                                                                                                      WPI; 1999-045171/04.
                                                                                                                                                                                                                                                              Barash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis genome contig SEQ ID NO:261.
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Percent Similarity:
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Query Match:
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                                                                                                                                                  US-10-008-355-25
                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                   commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for disquosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome AAXI2938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with
                                                                                                                                                                                                                                                                                                                                   Sequence 4951 BP;
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-Q-/cgn2_1/USPTO_Spool/US10008355/runat_17122002_112337_14593/app_query.fasta_1.398
-DB=-GenEmbl -OEMT=fastap -SUFFIX=p2n.rge -MINATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END--1 -MARIX=DSum62 -TRANS-human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -NODE=LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10008355_eCGN_1_1_1616_@runat_17122002_112337_14593 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XCAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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                                               DNA encoding V8 protease
E03836
E03836.1 GI:2172050
JP 1992211370-A/2.
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S. aureus
D00730
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Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from Staphylococcus aureus ATCC 12600 Biochim. Biophys. Acta 1121 (1-2), 221-228 (1992)
                         Staphylococcus aureus
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  Staphylococcus aureus
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/db_xref="taxon:1280"
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Query Match:
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Patent: JP 1992211370-A 1 03-AUG-1992;

SHIONOGI & CO LTD

OS Staphylococcus aureus

PN JP 1992211370-A/1

PD 03-AUG-1992

PD 03-AUG-1992

PR 19-FEB-1991 JP 1991024633

PR 20-FEB-1990 JP 90P 40398
                                                                                                        Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 1586)
Nakamura, E., Tamaki, M., Teraoka, H., Matsumoto, K., Fujiwara, K., Tsuzuki, H., Yoshida, N. and Kakudou, S
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DNA encoding V8-like protease.
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                                                                                                NEW PROTEASE
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19-FEB-1991 JP 1991024633
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NAKAMURA ETSUO, TAMAKI MIKIO,
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*source: clone=pAM82SIGV8;
Feature is identified by similarity;
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hypothetical: No;
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/db_xref="taxon:1280"
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Staphylococcus aureus.
Staphylococcus aureus
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                                                                                                                                                                     Nucleotide sequence of the serine protease gene of Staphylococcus aureus, strain V\boldsymbol{\theta}
                                                                                                                                                                                            South San Francisco, CA
2 (bases 1 to 1634)
Carmona,C. and Gray,G.L.
                                                                                                                                                                                                                      South San Francisco, CA
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Staphylococcus aureus
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*source: clone=pAM82SIGV8;
Feature is identified by experimental;
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Location/Qualifiers
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/db_xref="taxon:1280"
302 c 219 g 476 t
/transl_table=11
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                      /codon_start=1
                                    /note="preproenzyme (AA
                                                             clone="pV8CO"
                                                                        /db_xref="taxon:1280'
                                                                                    /strain="V8"
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Staphylococcus a
AF309515
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Infect: Immun. 69 (1), 159-169 (2001)
                                                                                                                                                                                                                                                                           Submitted (28-SEP-2000) Laboratory Medicine and Pathobiology, University of Toronto, Sunnybrook and WCHSC, 2075 Bayview Avenue, Toronto, ON M4N 3M5, Canada
                                                                                                                                                                                                                                                                                                                                                                                 20569178
11119502
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Rice, K.C. and McGavin, M.J.
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1 (bases 1 to 3240)
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/db_xref="taxon:1280"
354. .2994
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354. .557
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SKQQTPKIQKGGNLKPLEQREHANVILPNNDRHQITDTTNGHYAPVTYIQVEAPTGTF
IASGVVVGKDTLTTNKHVVDATHGDPHALKAPPSAINQDNYPNGGFTABGDITKYSGED
DLAIVKFSPNEQNKHIGEVVKPATMSNNAETQVNQNITVTGYPGDKPVATMWESKGKI
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/note="twelvefold repeated tripeptide (Pro-Asp-Asn)"
                                                                               endopeptidase'
                                                                                                                                  /gene="sspA"
354. .1364
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/db_xref="SWISS-PROT:P04188"
/protein_id="AAG45843.1"
/db_xref="GI:12025238"
                             /product="SspA"
                                                /transl_table=11
                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                 /codon_start=1
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AJ293885.2 GI:22218025
Cysteine proteinase; glutamyl endopeptidase;
proD gene; proM gene; spwl gene.
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/note="encodes :
2665. .2994
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2103. .2624
/gene="ssp8"
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SKQQTPKIQKGGNLKPLEQREHANVLLPNNDRHQLTDTTNGHYAFVTY LQVEAPTGTF
IASGVVVGKDTLLTNKHVVDATHGDPHALKAFPSAINQDNIPNGGFTAEQITKYSGEG
DLAIVKFSPNEDNKHIGEVVKFATMSNNAETQVNQNITVTGYPGDKPVATMWESKGKI
TYLKGEAMQYDLSTTGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQ
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/codon_start=1
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EDQVQYENTLKNFKIREQQFDNSWCAGFSMAALLNATKNTDTYNAHDIMRTLYPEVSE
QDLPNCATFPNQMIEYGKSQGRDIHYQEGVPSYEQVDQLTKDNVGIMILAQSVSQNPN
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INVKSDKVPQKVKDLAQQQFAGYAKALDKQSNAKTGKYELGEAFKIYKFNGEEDNSYY
YPVIKDGKIVYTLTLSPKNKDDLNKSKEDMNYSVKISNFIAKDLDQIKDKNSNITVLT
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/product="SspC"
/protein_id="Nad45845.1"
/protein_id="Nad45845.1"
/db_xref="GI:12025240"
/translation="MYQLOFINLYXDTTKLTHLEQTNINLFIGNWSNHQLQKSICIRH
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1554. 2624
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/protein_id="AAG45844...
/db_xref="GI:12025239"
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Submitted (30-AUG-2000) Kakikawa M., Molecular Biology Group,
Toyama University, 3190 Gofuku, Toyama, 930-8555, JAPAN
revised by author (08-AUG-2002)
On Aug 13, 2002 this sequence version replaced gi:9968802.
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Yamakawa,A., Taketo,A. and Kodaira,K.I.
Genetic and biochemical characterization of glutamyl endopeptidase
of Staphylococcus warneri M
Gene 281 (1-2), 115-122 (2001)
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Submitted (06-MAR-2002) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8423, Fax:81-3-3481-8424)
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Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
Yamamoto,K. and Hiramatsu,K.
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Aoki,K., Oguchi,A., Nagai,Y., Asano,K.,
Kuroda,M., Hiramatsu,K. and Kikuchi,H.
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Lancet 359 (9320), 1819-1827 (2002)
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MW0823"
                                                                                                                                                                                                                  'codon_start=
                                                                                                                                                                                                                                                      /gene="MW0826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORFID:MW0825"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="ORFID:MW0823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="MW0823"
                                                                                                                                                                                                                                     'note="ORFID:MW0826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, similar to NADH dehydrogenase"
                                  .6429)
                                                                    . 6429)
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/translation="MMFKLNNTLSNEINTLIGIPEHLNOLERISHNHIDITESLERL
KHQHIIGSKVOKIYTTAFDVODOTYRLLTYVGLONLKTKIKIKIKGHLFQYIKSEH
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VEVMNTDAEGRLVLADAVFYANQYQPSVIMDFATLTGAAIVALGDDKAAAFESNSKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLLPYGFGQIFQQIIQSGFAKANHPIEFNMIWKAMLIPSMGYIVGLLIGLYVYRKPRE
YETRKISDSDNVTELKPYILIVTIVAILATFLVQTFTDSMIFGALAGVLVFFISRAYN
WYELDAKFVEGIKIMAYIGVVILTANGFAGVMNATGDIDELVKTLTSITGDNKLFSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNDILQISSEVDEMVFELPITATERASIKHSDIADLVNHTNGQGKALFAASFVTHFSG
QTPHIHFDIAGPATTNKASYNGPKGPTGFMIPTIVQWLKQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSYLEDRGVEFKIATPIVACNEKGFVVEVDGEKQQLNAGTSVWAAGVRGSKLMEESFE
GVKRGRIVTKQDLTINGYDNIFVIGDCSAFIPAGEERPLPTTAQIAMQQGESVAKNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="maqdrkkvlvlgagyaglqtvtklqkaIsteeaeItlinkneyh
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LGETACSLGSANLIDTTKFIPLGLEMNANHIHSAKDGHVTATAEIIHQGKSTHVWDIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMYVIGLIVTLGIGSSFATIPIIASLFIPFGASIGLDTMALIALIGTASALGDSGSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVFGKNIVDGAEVALSYALLGGFAALISYSGITDYLVGKIINAIHAENSRWSRVKVK
VTIIIALLAMSIMSQNLIPVHIAFIPIVIPPLLSLFNDLKIDRRLIGLIIGFGLCFPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RILNGESTEEFEYVDRGTVCSLGSHDGVGMVFDKPIAGKKAAFMKKVIDTRAVFKIGG
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STLGAMSLLFGFFLYFTATQGFVNMQLIVAIIFVLITGFLSSHMIMKAAYNIKTPYTK
KTKVDEISEDLKDTKL"
                                                                                             complement(9275./gene="mnhC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(7786...9282)
/gene="mnhD"
complement(7786...9282)
/gene="mnhD"
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/gene="mnhF"
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/gene="mnhG"
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/gene="mnhG"
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TPITQISDGLINTENNSVPYQQIMVATGFEQDFMSQPLIKQLIQNYDAPINECNYPVI
SEKLEWIPNLFYAGCFADLELGPFGRNVMGGRKAAERIEQAFLKLQQYSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTNRIEMPYLRSPIVHHVHPQPFHLKQFAKQHQYTNAFYGPYQRPELTMFMDHIAHAS
KQYQLEDCLVQGLVQTLDKQEDKWHIKLEDGQIITTDCVVIAIGSTNIPFMPDILKDK
QNVNHIFEKEHDQVVYDKTDHIVGSGITAAHLALKLLNHDNDKKIHLWLNKDIEIHDF
                                                                                                                                                                                                                                              LHDMLVKLALFLLIGIMIKITGTADLRQFGGLIKRYPVLGWSFFIAALSLAGIPPLSG
FYGKFFIVQSTFERGFYLSGVIVLLSSLVVLYSVIRIFLQGFFGQPKGYDLNNKVDVK
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/gene="mnhE"
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/protein_id="BAB94694.1"
/db_xref="GI:21203996"
/translation="MNHNVIIVIALTIVVISMLAMLTRVVLGPSLADRVVALDAIGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
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/db_xref="GI:21203994"
                                                                                                                                                                                               YLTTIAIVAVVITVLYGLSADYLYPMVKAGAETFYNPSTYVKAVLGGK"
                                                                                                                                                                                                                                                                                                                                                 YVILFLALLTIIFGCVGAVAYANIKKIILYNVMIAVGVILVGVAMMTESGMIGAIYYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mAVQLVLNFIIAVFWLFVTNSYTTNNFVLGFIFGLVLVYLLHRV
LPGRFYVITLYRIIKLVIIFLIELIKANFDVLKIIIKPSIKNEPGFFVYHTDLKKDWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Na+/H+ antiporter subunit"
/protein_id="BAB94695.1"
/db_xref="GI:21203997"
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/transl_table=11
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/transl_table=11
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FEATURES
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Best Local Similarity:
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MEDLINE
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                                                                                                                                          JOURNAL
                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                            AUTHORS
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21311952
Technology and Evaluation, Biotechnology Center; 2Chome 49.
Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
(E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-8423, Fax:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13700734.
Location/Qualifiers
                                                                                                                                                             Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H. Direct Submission
                                                                                                                                                                                                                                                                                                                                        Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I., Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M. Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A., Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C., Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J., Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K. Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus subsp. aureus N315 (sub_spe
strain:N315) DNA.
Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome, section 4/10.
AP003132 BA000018
AP003132.2 GI:14349174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus subsp. aureus N315 genomic DNA,
                                                                                                                Submitted (30-JAN-2001) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10
                                                                                                                                                                                                                                                                                                                          aureus
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                                                                                                                                                                                                                                 (bases 1 to 298050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Na+/H+ antiporter subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMGGLKHGTVPIYEANVKSYVDPIPQALILTAIVIAFATTAFFLVLAFRTYKELGTDN
VESMKGVPEDD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="mnhB"
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3367. .4542
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3367. .4542
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3134. .3370
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FDKPFKAKNIKDFWNRWHMTLSFWFRDCIYMRSLFYMSRKKLLKSQFAMSNVAFLINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448. .1905
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JOURNAL
MEDLINE
REFERENCE
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AUTHORS
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VERSION
KEYWORDS
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                                                                                                                    Direct Submission
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan (E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454, Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13875305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus:
sequence, section 4/9.
AP003361 BA000017
AP003361.2 GI:1424676
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphy.
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7973. .9181
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1. .347235
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                                                                                                                                                                                                                                                                                                                                                              (9264), 1225-1240 (2001)
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VLTARSKGLSMNKIYNKHILRNSLIPIITFLGADIVSILGGAVITETIFSYNGIGKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="pligopeptide transport system ATP-binding protein AppF homologue"
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HISDVIGVMYLGHIVEIASDKEIYENPKHPYTKALISSIPQIDKHNNNRIILKGELPS
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6783. .7769
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NPITTEFEDLLYMVDGTYYYAVHFDSHVDQEVINDSYSQLLEFAYPTDRTEVYLNDYA
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5943. .6662
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EFGHSAHSYFSRKFQPSNSSDYTIFVAEVASTCNEALLSDYMDKHLDDEKRLLLLNQE
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5177. .5572
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7817. .9625
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LERFRATLFRQTMFAEFEHKIHAIEEAGEPLTPTRMNEEYAKLNKLYFGDSVETDED:
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Direct Submission
Submitted (19-JAN-2001) Dubin G., Institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dubin, G., Chmiel, D., Mak, P., Rakwalska, M., Rzychon, M. and Dubin, Molecular cloning and biochemical characterisation of proteases from Staphylococcus epidermidis
Biol. Chem. 382 (11), 1575-1582 (2001)
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/gene="yjbM"
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/strain="6746"
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Location/Qualifiers
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/db_xref="taxon:32630"
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/product="extracellular serine
/product="extracellular serine
/evidence=experimental
/evidence=204 t
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NEHNQHIGQVVKPATISSNTDTRINENITVTGYPGDKPLATMWESVGKVVYIGGEELR
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                       Query Match:
                                                                                                                Alignment Scores:
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2 Taylor, J. David., Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and Fuchon, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3189 bp
Sequence 3694 from Patent WO0134809
AXI44972
                                                                                                                                                                                                                                                                                                                                                         synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 3189)
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1 (bases 1 to 318)

Kimmerly, M.J., Taylor, J. David., Nelsen, A.J., Godlevski, M.M.,

Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,

Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,

Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and

Furdon, P.J.
                                                                                                                                                                                                                                                                                       GLAXO
                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis nucleic acids Patent: WO 0134809-A 3694 17-MAY-2001;
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/strain="SRI"
/db_xref="taxon:1282"
/clone="step.1015e12"
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                                                                                                                                                                      /note="synthetic nucleic acid sequence"
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                                                                                                                                                                                                           /organism="synthetic construct"
/db_xref="taxon:32630"
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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                     FEATURES
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MEDLINE
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                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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gene
                                                                                                                                                                                                                                                                                 Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S.,
Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,M.C.,
Frohme,M., Furlan,L.R., Garnier,M., Goldman,G.H., Goldman,M.L.,
Gomes,S.L., Gruber,A., Ho,P.L., Hoheisel,J.D., Junqueira,M.L.,
Kemper,B.L., Kitajima,J.P., Krieger,J.E., Kuramae,E.E., Laigret,F.,
Lambais,M.R., Leite,L.C.C., Lemos,E.G.M., Lemos,M.V.F., Lopes,S.A.,
Madeira,A.M.B.N.,
Marchado,J.A., Machado,M.A., Madeira,A.M.B.N.,
Madeira,H.M.F., Marino,C.L., Marques,M.V., Martins,E.A.L.,
Martins,E.M.F., Matsukuma,A.Y., Menck,C.F.M., Miracca,E.C.,
Miyaki,C.Y., Monteiro-Vitorello,C.B., Moon,D.H., Nagai,M.A.,
Mascimento,A.L.T.O., Netto,L.E.S., Nhani Jr.A., Nobrega,F.G.,
Nunes,L.R., Oliveira,M.A., de Oliveira,M.C., de Oliveira,R.C.,
Palmieri,D.A., Paris,A., Peixoto,B.R., Pereira,G.A.G., Pereira
Jr.,H.A., Pesquero,J.B., Quaggio,R.B., Roberto,P.G., Rodrigues,V.,
de M. Rosa,J.J., de Rosa Jr.,V.E., de Salva,F.R., da Silva,A.M., Silva
Sawasaki,H.E., da Silva,A.C.R., de Salva,F.R., da Silva,A.M., Silva
Jr.,W.A., da Silveira,J.F., Silvestri,M.L.Z., Siqueira,W.J., de
Souza,A., de Souza,A.P., Terenzi,M.F., Truffi,D., Tsai,S.M.,
Vettore,A.L., Zago,M.A., Zatz,M., Meidanis,J. and Setubal,J.C.
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2 (bases 1 to 10689)
Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvarenga, R., Alves, L.M.C., Araya, J.E., Baita, G.S., Baptista, C.S., Barrenga, R., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S. Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simpson, A.J., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvas, L.M., Araya, J.E., Baia, G.S., Baptista, C.S., Barvarenga, R., Alves, L.M., Araya, J.E., Baia, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R., Bueno, M.R., Camargo, A.A., Camargo, L.E., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C., Costa-Neto, C.M., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-Dorry, H., Facincani, A.P., Ferreira, A.J., Ferreira, V.C., Ferro, J.A., Fraga, J.S., Franca, S.C., Franco, M.C., Frohme, M., Furlan, L.R., Garnier, M., Goldman, G.H., Goldman, M.H., Gomes, S.L., Gruber, A., H., P.L., Hohelsel, J.D., Junqueira, M.L., Kemper, E.L., Kitajima, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carrer,H., Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C.R., Costa-Neto,C.M., Coutinho,L.L., Cristofani,M., Dias-Neto,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylella fastidiosa 9a5c, section 154 of 229 of the complete genome AE004008 AE003849
                                                                                                                                                                                                          Submitted (02-JUN-2000) Organization for Nucleotide Sequencing Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The genome sequence of the plant pathogen Xylella Xylella fasticiosa Consortium of the Organization
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                                                                                                                                                                                                                                                                        Submission
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alignment coverage: 88.0 %/subject alignment coverage:
105.0 %); identified by sequence similarity; putative; OR
located using Glimmer/RBSfinder"
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similarity; putative; ORF located using
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/gene="XF1872"
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/gene="XF1872"
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/gene="XF1871"
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/protein_id="AAF84677...
/db_xref="GI:9106962"
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/protein_id="AAF84679.1"
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similarity; putative; ORF located using
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Best Local Similarity:
Query Match:
           US-10-008-355-25 (1-10)
                                                                                                                                                   Percent Similarity:
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similarity; putative; ORF located using Glimmer/RBSfinder"
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SVILDTDLGGLVRSDPSTVNAVLTDSQTGAVLLTPEITVSALNKLRRSLEDELKASHAP
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similarity; putative; ORF located using Glimmer/RBSfinder"
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/gene="XF1878"
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AYIAGGFRGVKNV"
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similarity; putative; ORF located using Glimmer/RBSfinder"
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/gene="XF1877"
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/gene="XF1876"
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SSSVSLSSSVSSAPILGSSSVPSSH"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                           * NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Champerlata,J., Campoplano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cock,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 66762)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-10F17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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AC121125.1 GI:20800264
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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39829: contig of 717 bp
129: gap of 100 bp
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41453: contig of 714 bp
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38191: contig of 724 bp
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42275: contig of 722
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40639: contig of 710 bp
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13717 13816: gap of 100 bp 13817 14539: contig of 723 bp 14540 14639: gap of 100 bp 14640 15344: contig of 705 bp 15345 15444: gap of 100 bp 1545 16157: contig of 713 bp

16257: gap of 100 b 16968: contig of 711 17068: gap of 100 b 17781: contig of 713

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17881: gap of 100 bp 18602: contig of 721 bp

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06 6422; contig of 717 bp
23 6522; gap of
23 6722; gap of
24 7192; contig of 670 bp
25 7292; gap of
26 100 bp
27 8806; contig of 709 bp
27 8806; contig of 705 bp
28 806; contig of 714 bp
27 9720; gap of
28 9620; contig of 714 bp
28 1016; contig of 686 bp
29 10506; gap of
20 10506; gap of
21 100 bp
31 11332; gap of
31 100 bp
31 11332; gap of
31 100 bp

100 bp of 714 bp

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7192: contig of 670 bp in 92: gap of 100 bp 92: gap of 100 bp 101: contig of 709 bp in 1 10: gap of 100 bp 10: gap of 10: ga

18703 18772: gap of 100 bp
18703 19399: contig of 697 bp
19400 19499: gap of 100 bp
19500 20231: contig of 732 bp
20232 20331: gap of 100 bp
20232 21336: contig of 705 bp
21032 2136: gap of 100 bp
21137 21862: contig of 726 bp
21137 21862: contig of 726 bp
21137 21862: contig of 739 bp
2163 21962: gap of 100 bp
2163 22701: contig of 739 bp
22702 23801: gap of 100 bp
23514 23613: gap of 100 bp
23514 23613: gap of 100 bp
23514 23613: gap of 100 bp
23614 2426: contig of 712 bp
24327 24226: contig of 713 bp

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24426: 25244:

26: gap of 100 k 25144: contig of 718

25960: rr

100 k f 716

45 25960: contig of 716 bp
61 26078: contig of 718 bp
61 26778: contig of 118 bp
79 26878: gap of 100 bp
79 27574: contig of 100 bp
75 27674: gap of 100 bp
75 27674: gap of 722 bp
75 28396: contig of 722 bp
76 28396: contig of 722 bp
77 28173: contig of 677 bp
78 29173: gap of 100 bp
78 29173: gap of 100 bp
78 29173: contig of 677 bp
78 29173: contig of 729 bp
79 29173: gap of 100 bp

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30102: gap of 1 30825: contig of

30925:

723 100 k 722

925: gap 31647: с

Db 57225 ACAGGAAATAACAGCGGCTCTCCCCTATTT 57254

Search completed: December 20, 2002, 15:01:46 Job time : 1615.74 secs

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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/Cgn2_1/USPTO_spool/US10008355/runat_17122002_112337_14581/app_query.fasta_1.398
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=hunan40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Copyright (c) 1993 - 2002 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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first 45 summaries
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APPLICATION NUMBER: |
FILING DATE: 09-APR-
PRIOR APPLICATION DATA:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1018
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CITY: Palo Alto
                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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o. 542814		equence 1, Appl	equence 1, App	e 1, App	: 1, App	22, Ap	23, Ap	e 7, App	e 2, App	, Ap	e 1, App	1,	1,	1,	3, Appl	1,	21,	21,	35,	38	118	32,	11,	21,	28,	28,	28,	31,	31,	31, App	6, Ap	8, Appl

ALIGNMENTS

Sequence 726, Application US/09221017B
Sequence 726, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES. 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM.TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION NUMBER: US/09/221,017B
FILING DATE: 33-DEC-1998
CLASSIFICATION UNMBER: PP1182
FILING DATE: 31-DEC-1998
PRIOR APPLICATION DATA:
APPLICATION D

ATTORNEY/AGENT INFORMATION:

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                     : NUMBER OF SEQ ID NOS: 5674

: SEQ ID NO 892

: LENGTH: 936

: TYPE: DIA

: ORGANISM: Staphylococcus epidermidis

US-09-134-001C-892
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                                                            US-10-008-355-25 (1-10) x US-09-134-001C-892 (1-936)
                                                                                                            Query Match:
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                                                                                                                          Best Local Similarity:
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                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 892, Application US/09134001C
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1524 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1553
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HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
TYPE: nucleic acid
TYPE: formalist double
TYPO/IOGY: circular
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                                                                                                                                                                          NO . .
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TELEFAX: bou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 1...1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThrGlyGlyAsnSerGlySerProValPhe 10
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100.00%
100.00%
90.74%
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                                              US-10-008-355-25 (1-10) x US-09-221-017B-1045 (1-2384)
                                                                                                  Best Local Similarity:
Query Match:
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                                                                                                                               Percent Similarity:
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APPLICANT: ROSS, BRUCE C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP15:
FILING DATE: 30-JAN-1998
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                     ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650-610 0792
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1 ThrGlyGlyAsnSerGlySerProVal 9
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31-DEC-1997
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Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:

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                                                                                                                                                                                                                                                                                                                       US-10-008-355-25 (1-10) x US-09-071-035-427 (1-758)
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Best Local Similarity:
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                                                                                                                                                                             Sequence 425, Application US/09071035 Patent No. 6448043
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gil H. Choi
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APPLICANT: Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 427:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A Anders Brookes
REGISTRATION NUMBER: 36,3;
                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          575 ACCGCCGCTCAATCTGGTTCACCAATCTAT 604
               STREET: 9410 Key CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 ACCGGCGGCAACTCAGGCAGTCCGGTC 446
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CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                          ADDRESSEE:
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20850
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                                                             9410 Key West Avenue
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                                                                            Human Genome Sciences,
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90.00%
70.00%
81.48%
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Patent No. 5459064
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER: EPSON PC-286 Book ty
COMPUTER: EPSON PC-285 Book ty
OPERATING SYSTEM: MS-DOS 2.11
                                                                                                                                                                                                                                                                                              STREET: 540 ....
STREET: Menlo Park
CITY: Menlo Park
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,372
FILING DATE: 24-0CT-1991
APPLICATION NUMBER: Japanese Patent
APPLICATION NUMBER: Application No.
FILING DATE: October 24, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               SOFTWARE: Wordstar 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SHIONOGI & CO., LTD.
TITLE OF INVENTION: A NO. 5459064el Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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NAME: A. Anders Brookes
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OPERATING SYSTEM:
SOFTWARE: ASCII 1
                                                                                                                              FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                 APPLICATION NUMBER:
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BOZICEVIC, KARL
                                                                                                                                                                                                                                                                                                                                                   545 Middlefield Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (301)
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                                                                                                                                                                                                                                                                                                                                                                    Morrison & Foerster
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301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
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44.00
90.00%
70.00%
81.48%
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                                                                                                                                                                 US/08/035,634
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                                                                                                                                                                                                                                Book type laptop
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Matches:
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Indels:
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                                                5459064 2-288110
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7000

REGISTRATION NUMBER:

28,807

29900-20298.00

REFERENCE/DOCKET NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 856, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 677-7522
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESSPONDENCE ADDRESS:
CORRESSPONDENCE ADDRESS:
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 GGAGGACAAAGCGGTTCACCGGTATTC 1120
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LENGTH: 1448 base pair:
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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LOCATION: 323 to 1270
IDENTIFICATION METHOD: by experiment
NAME/KEY: signal peptide
LOCATION: 323 to 604
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                                                                                                                                                         COUNTRY:
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   APPLICATION NUMBER:
                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                         Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                       Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Philippsen, Peter
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                                                                                                                                                                                                                                 6239264artis Corporation
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43.00
88.89%
88.89%
79.63%
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US/08/998,416
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Matches:
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Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                              TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Russell, D
APPLICANT: Thigpen, A
TITLE OF INVENTION: E
TITLE OF INVENTION: E
NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . No.:
                                                               NAME: Corder, Timothy S.
REGISTRACION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: UR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,169
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
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ORIGINAL SOURCE:
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LENGTH: 743 base pairs
TYPE: nucleic acid
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                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Corder, Timothy S.
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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ADDRESSEE: Arnold, White & Durkee
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                      Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08626169
                                                                                                                                                                                                                                                                                                                                                                      Texas
                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 4433
240 base pairs
                                                                                                                                                                                                                                                                                                                                                    United States
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60.00%
74.07%
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Anice E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOMARKERS FOR DETECTION, DIAGNOSIS AND PROGNOSIS OF PROSTATE CANCER 19
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Matches:
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Best Local Similarity:
Query Match:
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US-09-164-907-2
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo sapiens
US-09-164-907-2
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APPLICANT: RUSSELL, DAVID W.
APPLICANT: THIGPEN, ANICE E.
APPLICANT: THIGPEN, ANICE E.
TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER
FILE REFERENCE: URCO: 021
CURRENT APPLICATION NUMBER: US/09/164,907A
CURRENT FILING DATE: 1998-10-01
CURRENT FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 08/626,169
EARLIER FILING DATE: 1906-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 19 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2 LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5447862 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application Patent No. 5447862
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                        APPLICANT: Kester, Hermanus Cornelis Maria TITLE OF INVENTION: No. 5447862el Expression System NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                 APPLICANT:
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STRANDEDNESS: single
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                                               ADDRESSEE: CIBA-GELGE CONTROL OF THE CONTROL OF THE
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                                 Hawthorne
New York
                                                                                                                                                                                                                                                                         Meyhack, Bernd
Gysler, Christof
Visser, Jacob
                                                                                                                                                                                                                                                                                                                                                                                    Heim, Jutta
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39.00
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Matches:
Conservative:
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Matches:
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Indels:
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STRANDEDNESS: do
TOPOLOGY: linear
MOLECULE TYPE: DNP
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Aspergillus niger N400
IMMEDIATE SOURCE:
CLONE: Plasmid pGW830 (DSM 4389)
                                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-JUL-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 8818046.8 FILING DATE: 28-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21 CLASSIFICATION:
                                                                   LOCATION:
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COMPUTER: I
NAME/KEY:
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DEDNESS: double
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1194..1337
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1599..1725
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1543..1598
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1400..1542
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1338..1399
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1134..1193
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Alignment Scores: Pred. No.:
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Best Local Similarity:
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CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 123
LENGTH: 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 123, Application US/09222575 Patent No. 6387697
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer TITLE OF INVENTION: and Methods for Their Use FILE REFERENCE: 210121.470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                 LOCATION: (373)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
                                                                   LOCATION: (502)
OTHER INFORMATION: Where
                                                                                                          LOCATION: (496)
OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                        LOCATION: (482)
OTHER INFORMATION: Where n
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OTHER INFORMATION: Where n
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2170..2502
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Conservative:
Matches:
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Best Local Similarity:
Query Match:
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                          Best Local Similarity:
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                                       Percent Similarity:
                                                      score:
                                                                   Pred.
                                                                              Alignment Scores:
                                                                                                          US-07-624-313-3
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Patent No. 5250411
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                              NAME: Ryan, John W.
REGIETION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8515
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8904100-8
FILING DATE: 05-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                            ANTI-SENSE:
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                                                                                                                                                                                                                                                                                    TELEPHONE: 212-0-
TELEPHONE: 212-354-8113
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                               STRANDEDNESS:
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DEDNESS: both
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            Mismatches:
Indels:
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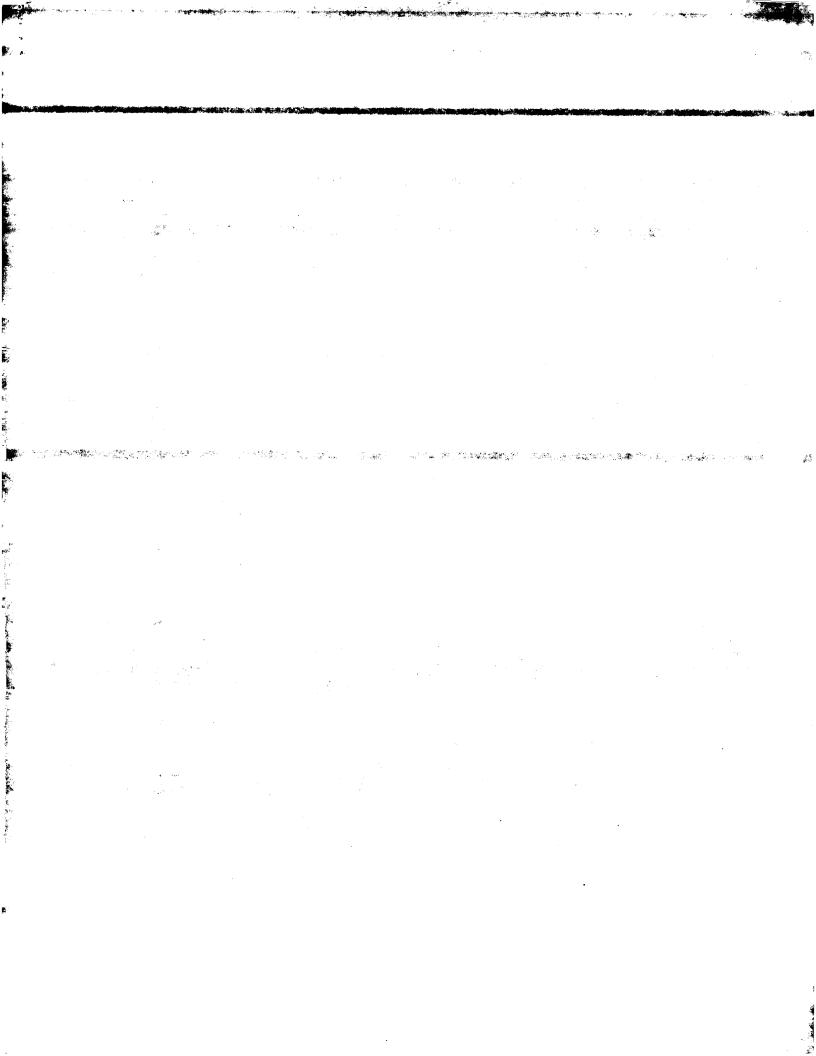
Gaps:

US-10-008-355-25 (1-10) x US-07-624-313-3 (1-663)

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Pred. No.:
                                       Alignment Scores:
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Best Local Similarity:
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                                                                                    US-09-061-709-6
                                                                                                                                                                  SEQ ID NO 6
LENGTH: 3412
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APPLICANT: Knuth, Alexander
APPLICANT: Cld, Lloyd J.
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                    APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Muth, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/061,709B CURRENT FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3283
TYPE: DNA
                                                                                                                     ORGANISM: Homo
                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 GGAGGAAACAGTGGGAAACCTGGATTT 194
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38.00
90.00%
70.00%
70.37%
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38.00
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Length:
Matches:
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US-10-008-355-25 (1-10) x US-09-061-709-6 (1-3412)
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US-08-225-224-31/c
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Вþ
                                                                    US-10-008-355-25 (1-10) x US-08-225-224-31 (1-39)
                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                         ; MOLECULE TYPE: US-08-225-224-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Steurico
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600 TELEFAX: (415) 543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PASTAN, Ira
APPLICANT: KREITMAN, KOBERT J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2535 ACTCACGGCAGTTCTGGATCACCTGTGTAT 2564
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                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105-1493
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24 ACCGGAGGTAACGGTGGGGCACCT
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                                1 ThrGlyGlyAsnSerGlySerPro
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Search completed: December 20, 2002, 14:11:50 Job time: 42.4211 secs



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Command line parameters:

MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgp2_1/USPTO_Spool_VSI0008355/runat_17122002_112339_14635/app_guery.fasta_1.398
-QB-Published_Applications_NA -QFMT-fastap -SUFFIX=p2n.rnpb -MINMATCH+0.1
-LOOPEXT-0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.dd -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MXX=100
-THR_MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10008355_eCGN_11_21_erunat_17122002_17239_14635
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NCES_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB
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Perfect score:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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Listing first 45 summaries
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99.214 Million cell updates/sec
Sequence 1, Appli
Sequence 261, App
Sequence 327, App
Sequence 1705, Ap
                                                                                Description
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5 40 74.1 7441 10 US-09-764-878-243 Sequence 243, App 77.2 235 10 US-09-860-755-7672 Sequence 5672, Ap 77.2 217.5 9 US-10-01-887-75 Sequence 5672, Ap 78.2 217.5 9 US-09-764-868-111 Sequence 683, App 17.2 217.5 9 US-09-764-868-111 Sequence 683, App 17.2 232.5 10 US-09-815-343-1415 Sequence 683, App 17.2 232.5 10 US-09-815-343-1285 Sequence 683, App 17.2 232.5 10 US-09-815-343-1285 Sequence 683, App 17.2 232.5 10 US-09-815-343-1285 Sequence 683, App 18.3 70.4 218 10 US-09-815-343-1285 Sequence 683, App 18.3 70.4 222 10 US-09-815-343-1285 Sequence 683, App 19.4 243 10 US-09-815-343-1285 Sequence 683, App 19.4 244 10 US-09-815-343-1285 Sequence 5210, App 19.5 10 US-09-815-343-1285 Sequence 5210, App 19.5 10 US-09-815-343-1285 Sequence 683, App 19.5 10 US-09-815-123 Sequence 6501, App 19.5 10 US-09-808-701-123 Sequence 6501, App 19.5 10 US-09-808-701-123 Sequence 123, App 19.5 10 US-09-808-701-123 Sequence 6501, App 19.5 10 US-09-808-701-13 Sequence 6501, App 19.5 10 US-09-808-701-13 Sequence 6501, App 19.5 10 US-09-808-701-13 Sequence 133, App 19.5 10 US-09-808-701-153, App 19.5 10 US-09-808-701-153, App 19.5 10 US-09-808-701-1544, App 19.5 10 US-09-808-701-2444, App 19.5 10 US-09-808-701-2444, App 19.5 10 US-09-808-701-
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ALIGNMENTS

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Sequence 1, Application US/10008355

Patent No. US20020164759A1

GENERAL INFORMATION:

APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Potempa, Jan
SAPPLICANT: Potempa, Jan
SAPPLICANT: Potempa, Jan
SERIE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT FILING DATE: 2001-11-08
FRIOR APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2139
TYPE: DNA
ORGANISM: Porphyromonas gingivalis
US-10-008-355-1

Alignment Scores:
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
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US-09-974-300-327
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Best Local Similarity:
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US-09-070-927A-261
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                    RESULT
                                                                                                                                  US-10-008-355-25 (1-10) x US-09-070-927A-261 (1-4951)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 261:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                       695 ACCGGCGTCAATCTGGTTCACCAATCTAT 666
                                                                           1 ThrGlyGlyAsnSerGlySerProValPhe 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 4951 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB369 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-10) x US-10-008-355-1 (1-2139)
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; LOCATION: (1)...(450)
; OTHER INFORMATION: n =
US-09-867-701-1705
                                                  US-10-008-355-25 (1-10) x US-09-867-701-1705 (1-450)
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                                                                                                          Best Local Similarity:
Query Match:
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                                                                                                                                                 Percent Similarity:
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SEQ ID NO 327
LENGTH: 534
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 2101.21.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1705, Application Patent No. US20020132237A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05
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                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 450
TYPE: DNA
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ACAGGAGGTAATTCTGGCAAGCCC

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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-LIB34-067-Q1-E1-F7
US-09-960-352-5672
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US-09-864-761-9954/c
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Best Local Similarity:
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US-09-764-878-243/c
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NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 243
LENGTH: 7441
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LENGTH: 235
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APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
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ORGANISM: Homo sapiens
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Matches:
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SEQ ID NO 9954
LENGTH: 584
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Patent No.
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR APPLICATION NUMBER: PCT/US01/00662
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PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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OTHER INFORMATION: EXPRESSED IN HEAR
OTHER INFORMATION: EXPRESSED IN BRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
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3 GlyAsnSerGlySerProValPhe 10
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Indels:
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Conservative:
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-111
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                                                      US-10-008-355-25 (1-10) x US-09-764-868-111 (1-2109)
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Best Local Similarity:
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 111, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION:
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SEQ ID NO 75
LENGTH: 1775
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                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
NUMBER OF SED ID NOS: 137
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ORGANISM: Homo sapien
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75, Application U
5. US20020155464A1
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US-10-008-355-25 (1-10) x US-10-025-380-683 (1-3255)
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Best Local Similarity:
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LENGTH: 3255
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Xu, Jian
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APPLICANT:
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APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
                                                                                                                                                                  APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
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APPLICANT:
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APPLICANT:
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Stolk, John A.
Wang, Tongtong
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Wang, Aijun
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Smith, Carole Lynn
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Benson, Darin R.
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Vedvick Thomas S.
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Smith, Carole L.
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Benson, Darin R.
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Conservative:
Mismatches:
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APPLICANT: Wang, Aijun
APPLICANT: Clapper, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 683
LENGTH: 3255
TYPE: DNA
ORGANISM: Homo sapien
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 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER FILE REFERENCE: 2.10121.504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1415
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                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                              Sequence 1415, Application US/09815343 Patent No. US20010055596A1
                                                                                                                                                   APPLICANT: Xu, Jiangchun APPLICANT: King, Gordon E.
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US-09-815-343-676
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                                    SOFTWARE: FastSEQ
SEQ ID NO 1285
LENGTH: 222
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LENGTH: 222
TYPE: DNA ORGANISM: Homo sapien
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Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Weagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-815-343-1285

Alignment Scores: 27.4 Length: 222 Score: 38.00 Matches: 7 Percent Similarity: 90.00% Conservative: 2 Percent Similarity: 70.00% Mismatches: 1 Out Gaps: 0 Out Gaps: 0
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Post-processing: Minimum Match 0% Maximum Match 10
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1: /cgn2_6/ptodata/1,
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 US-08-523-373-22
US-08-523-373-23
US-08-523-373-24
US-08-657-192-3
US-08-657-192-9
US-08-657-192-9
US-08-657-192-9
US-08-657-192-9
US-08-657-192-15
US-09-134-011C-3729
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US-09-071-035-428
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PCT-US95-10661A-7
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16.940 Million cell updates/sec
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Compugen Ltd
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   22, Applia 24, Applia 3, Applia 6, Applia 7, Applia 8, Applia 7, Applia 8, A
                                                                 ; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: F
US-08-523-373-22
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US-08-523-373-22
                                                                                                                                                         APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-2
TELEPAN: 703-836-620
TELEPAN: 703-836-2021
INFORMATION FOR SEQ ID NO: 22:
Query Match
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Matches 10
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Patent No.
                                                                                                                                                                                                                                                                                                                                                     APPLICATION 05-SEP-1995
FILING DATE: 05-SEP-1995
CLASSIFFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-2
APPLICATION 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
NUMBER OF SEQUENCES: 24
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314-3187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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5. 6037145
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   Conservative
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                                                                                                    linear
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05-SEP-1995
                                                                               peptide
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US-08-245-294-8
US-08-307-279A-8
US-08-307-279A-8
US-08-307-279A-8
US-08-307-279A-1
US-08-868-373-8
US-08-96-791-2
PCT-US95-10661A-2
S268270-2
US-08-296-791-3
US-08-296-791-4
PCT-US95-10661A-4
US-08-296-791-4
US-08-296-791-4
US-08-296-791-4
US-08-296-791-5
US-08-296-791-5
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Score 54; DB Pred. No. 0.1
0; Mismatches
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                                DB 3;
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Sequence 3, Appli
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Sequence 6, Appli
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                                                                                                                                                                               US-08-523-373-24
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                                                                                                                 Sequence 24, Application US/08523373
Patent No. 6037145
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-N0Y-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-2:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
BITRNS. DOANE, SWECKER & MATHIS
                    APPLICANT: Yabuta, Masayuki APPLICANT: Obsuye, Kazuhiro TITLE OF INVENTION: PROCESS NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          165 TGGNSGSPVF 174
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CITY: Alexandria
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    ADDRESSEE:
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BURNS, DOANE, SWECKER & MATHIS
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                                        PROCESS FOR PRODUCTION OF PROTEIN 24
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US-08-657-192-3
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APPLICANT: YABUTA, N
APPLICANT: OHSUYE, F
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08657192 Patent No. 5747321
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Best Local Similarity
Matches 10; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 6-2
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-2
FILING DATE: 07-NOW-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
              CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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CURRENT APPLICATION DATA:
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CITY: A
                                                                                                                                                                                      STATE: Virginia COUNTRY: United States ZIP: 22313-1404
                                             APPLICATION NUMBER: FILING DATE: 03-JUJ
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TOPOLOGY: lir
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
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                                                03-JUN-1996
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MUTANT STAPHYLOCOCCUS AUREUS V8
PROTEASES
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JP 7-170086
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US-08-523-373-5
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                                                                                                          NFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 6
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                               APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yabuta, Masayuki APPLICANT: Ohsuye, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 TGGNSGSPVF 298
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                               TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                   REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 05-SEP
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STRANDEDNESS: si
TOPOLOGY: linear
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
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                                                                                                                                       703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BURNS, DOANE,
                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/523,373
05-SEP-1995
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                                             not relevant
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                                                                                                                                                                                                                                                                                         JP 6-238595
                                                                                                                                                                                 36,607
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Pred. No.
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RESULT 6
US-08-523-373-6
US-08-523-373-6
; Sequence 6, Application US/08523373
; Patent No. 6037145
; Patent No. 6037145
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                                                                                                                                                                                            Query Match
Best Local Similarity
"~+~hes 10; Conserv:
                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-523-373-6
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                                                                                         US-08-657-192-9
                                                                                                         RESULT 7
                                                            Sequence 9, Application US/08657192 Patent No. 5747321
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                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
    APPLICANT: YABUTA, APPLICANT: OHSUYE, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 6-238595 FILING DATE: 07-SEP-1994 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ohsuye, TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                   289 TGGNSGSPVF 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/O FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meuth, Donna M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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07-NOV-1994
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Kazuhiro
Masayuki
Kazuhiro
MUTANT STAPHYLOCOCCUS AUREUS V8
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Pred. No. 0.
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0.26;
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TITLE OF INVENTION:

PROTEASES

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LENGTH: 532 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-657-192-9
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth Donna M.
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 001560-264
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OP INVENTION: PROCESS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acid
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 836-6620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 TGGNSGSPVF 298
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CITY: Alexandria
                                FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                       ADDRESSEE: BUKNO, L. CTREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box CITY: Alexandria
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APPLICATION NUMBER:
                                                                    APPLICATION NUMBER:
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P.O. Box 1404
                                                                                                                                                                                                                       USA
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                                        05-SEP-1995
DN: 435
                                                                                                                                                                                                                                                                                                                                                   PROCESS FOR PRODUCTION OF PROTEIN
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                                                                    US/08/523,373
JP 6-238595
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В
; MOLECULE TYPE: US-08-657-192-15
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US-08-657-192-15
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1:
Patent No.
                                                                                                              TELEFAX: (703) 836-20; INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 7:
                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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APPLICANT:
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REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                               NAME: Meuth, Donna M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States ZIP: 22313-1404
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STATE: Virginia
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STRANDEDNESS: not
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                              TOPOLOGY:
                                            STRANDEDNESS:
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o. 5747321
                                                           amino acid
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P.O. Box 1404
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MUTANT STAPHYLOCOCCUS AUREUS V8
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Pred. No. 0.35;
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RESULT 11
US-08-332-562A-67
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LENGTH: 311
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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FILING DAIL.

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,457
APPLICATION NUMBER: 27-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             APPLICANT: BONADONNA, Lisa APPLICANT: HULETT, Mark D. TITLE OF INVENTION: FC REC
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 GGNSGSPVF 269
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les 9; Conservative
                                                                                        APPLICATION NUMBER: FILING DATE: 31-OC
                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                     D.C.
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3000 K Street, N.W.,
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HIBBS, Margaret L.
SCOTT, Bernadette M.
                                                                                                                                                                                                                                                                                                                                                                                    BONADONNA, Lisa
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                                                                                                     US/08/332,562A
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Pred. No. 0.35;
Mismatches
                                                                                                                                                                                                                                                                                    Suite 500
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Query Match
Best Local Similarity /u.v
Thes 7; Conservative
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Best Local :
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APPLICANT: Gil H.
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SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                            TELEFAX: (301) 309-851 INFORMATION FOR SEQ ID NO:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-3300
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VEI
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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TELEFAX: 904136
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                                                                                                                  STRANDEDNESS:
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CITY: Rockville
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les 9; Conserv
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STRANDEDNESS: si
                                                                                                         TOPOLOGY:
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                                                                                                                  single
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                                  81.5%;
70.0%;
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100.0%; Pred. No. 0.
tive 0; Mismatches
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                               Score 44; I
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                                            Length 252;
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                    Indels
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OPERATING SYSTEM: MSDOS
SOFTMARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                        APPLICANT: Budtz, Peter
APPLICANT: Nielsen, Per M.
TITLE OF INVENTION: PROTEIN PREPARATIONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55232370 No. 5523237disk of No.
STREET: 405 Lexington Avenue, 62nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELECHONE: (301) 309-8504
COMPUTER READABLE FORM
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COMPUTER: HP Vectra 486/33
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ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gil H. Choi
TITLE OF INVENTION: En
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               STATE: New York COUNTRY: United States of America ZIP: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                 CITY: New York
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CITY: Rockville
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70.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                 5523237th America, Inc
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RESULT 15
US-08-292-550-1
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/927,624
FILING DATE: 31 AUG 1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/DK91/006
FILING DATE: 8 MAR 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/DK
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,08
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 199/91
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 GGQSGSPVF 172
                                                                                                                           APPLICATION NUMBER: FILING DATE: 18 AUCLASSIFICATION: 42
                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                          STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 16-JU CLASSIFICATION: 43
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                Budtz, Peter
Mortensen, Steen B.
WENTION: A PROCESS FOR PRODUCING CHEESE
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88.9%;
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REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-292-550-1
Query Match
Best Local Similarity 88.9%; pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy 2 GGNSGSPVF 10
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Db 164 GGQSGSPVF 172

Search completed: December 20, 2002, 12:12:18
Job time: 19.3684 secs
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OM protein - nucleic search, using frame_plus_p2n model
                                                                                                          GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: Maximum DB seq length: -Q=/cgn2_1/USPTO_spool/US10008355/runat_17122002_112338_14609/app_query.fasta_1.398
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-MODEL=frame+_p2n.model -DEV=xlh Total number of hits satisfying chosen parameters: Searched: Scoring table: Run on: Database : Sequence: Perfect score: Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-10-008-355-25 54 December 20, 2002, 12:12:24; Search time 1521.05 Seconds (without alignments) 106.476 Million cell updates/sec 6: 7: 9: 10: 112: 113: 114: 116: 118: 16154066 seqs, 8097743376 residues BLOSUM62 TGGNSGSPVF 10 gb_est1:*
gb_est2:* em_htc:* em_estro:* em_estpl:* em_estmu: *
em_estov: * em_estin: * em_estba:* em_gss_rod:* em_gss_mam:* em_gss_vrt:* em_gss_fun:* em_gss_pln:* em_estom: * em_estfun:* gb_est4:* gb_est3:* gb_htc:* em_gss_pro:* em_gss_other:* em_gss_mus:* em_gss_inv:* em_gss_hum:* gb_gss:* gb_est5:* 0 20000000000 0.5 7.0 7.0 32308132

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

40 41 42 43 44	C 33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	c c 23 c 25 25 27	c 12 1134 1155 1177 1188 1199 1200 1200 1200	Result No
42 42 42 42 42	* 4 4 4 4 4 4 4 4 * * * * * * * * * * *		2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Score 47 47 47 46 45 45 45 45 45 45 45
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192 301 346 352 369 375	14544443377	075521	298 403 4432 4432 715 7158 813	73019971021 - #
13 9 9 14 12	19 11 12 11 10 11 10 11 11 11 11 11 11 11 11 11	17 12 14 12	13 10 10 10 11 11 11 11 11 11	DB 17 10 12 12 14 12 12 12 12
BI78 AA507 AA596 AA242 AA447 BM71 BF08	BB17684 BB176847 AW30847 AW31593 BG83482 BIS3030 BG38300 BJ19059 BG83453 BIS4522 AI608160	AQ91237 BF66888 BI69574 BQ88113 BE79475	BJ09991 AA47307 W72307 AW74356 AW74360 AL117983 AA175055 AL034929 BI44085 BG75112 BG75112	ID AA4119 BH400 BB622 BF694 AQ699 BO327 BG714 BF128 BF128 BF128 BF1893 AW060
17836 50730 59601 59601 24243 24704 44704 M7163 F0831	176886 BB176886 308476 3608 MAR 315936 13723 M 315936 13737 M 315937 60307342 830377 60307342 383001 300877 M 383001 30190590 BJ190590 BJ190590 834531 352788 M 545222 60318734	912379 nbeb0036 668889 60212329 695748 60334700 891134 AGENCOUR 794754 60159058	6126 kJ09991 6126 vh17d08. 307 zd60908.s 307 zd60908.s 43569 ur23d03 43569 ur23d03 4383 p9223a54 5055 ms82g01. 40854 ic77c12 51121 6027296 18747 6028192	cription 11980 zt65903. 400391 aG-ND-1652270 BB62270 694219 6020828 69991 HS_5334 327884 MR4-RT0 714149 6026745 714149 6026745 893687 QV1_MT0 060086 687001G

ALIGNMENTS

VEREVENCE	Decement of			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AA411980/c	RESULT 1
-	1	Mamma	Eukar	Homo	human	EST.	AA411	AA411	3', n	zt65g	AA411		

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B. 1980 1980.1 nRNA sequence. 1980 193.s1 Soares_testis_NHT sapiens GI:2070632 bp mRNA Homo sapiens linear E EST 12-AUG-1997 E IMAGE:727252

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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                             ACCESSION
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                   ACGGGAGGAAACTCTGGCAGTCCTATT 193
                                                                                                                                                                                                                                                                          DNA sequence
BH400391
               Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
Other_GSSs: AG-ND-147H4.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                               Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu
                                                                                                                                                                                                                                                                                                            426 bp DNA linear GSS 11-DEC-200 AG-ND-147H4.TF ND-TAM Anopheles gambiae genomic clone AG-ND-147H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Insert Length: 2072 Std Error: 0.00 Seq primer: -41ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu, Merck EST Project 1997
                                                                                                                                                                                                                          African malaria mosquito.
                                                                                                                                                                                                                                                             BH400391.1 GI:17346607
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Location/Qualifiers
Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:5924164"
/db_xref="taxon:9606"
/clone="IMAGE:727252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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47.00
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SOURCE
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VERSION
KEYWORDS
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BB622700
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Query Match:
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                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 2E 1 (bases 1 to 608)

E 1 (bases 1 to 608)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sasaki,C., Saki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tayawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

Muramatsu,M. and Hayashizaki,Y., RIKEN Mouse ESTS (Arakawa,T., et al. 2001)

Contact: Yoshihde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA, All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
,M., Konno,H., Okazaki,Y., Muramatsu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB622700 RIKEN full-length enriched, adult male olfactory brain musculus cDNA clone 6430525L24 5', mRNA sequence.
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                                                                                                                                      Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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Normalization and subtraction of cap-trapper-selected cDNAs
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/clone="AG-ND-147H4"
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                ayatsu,N., Sugahara,Y., Shibata,K.,
Muramatsu,M. and Hayashizaki,Y.
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mRNA sequence.
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                                        BF694219 611 bp mRNA linear EST 22-DI 602082842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared and sequenced in Mouse Genome Encyclopédia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
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/clone="6430525124"
/clone_lib="RIKEN full-length enriched, adult male
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/dev_stage="adult"
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ORGANISM
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                                                                                                                                                                                                                                                                     AQ699991 371 bp DNA linear HS_5334_A2_G04_SP6E RPCI-11 Human Male BAC Library genomic clone Plate=910 Col=8 Row=M, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1063 row: d column: 12
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (manualist)
                                          Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T. Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 371)
                                                                                                                                                                                                                                                  genomic clone
AQ699991
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Tissue Procurement: CLONETECH Laboratories,
Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                               AQ699991.1 GI:5390239
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/lab_host="DH10B (T] phage-resistant)"
/lab_host="DH10B (T] phage-resistant)"
/note="organ: muscle (skeletal); Vector: pDNR-LIB
/note="organ: muscle (skeletal); Vector: pDNR-LIB
/note="organ: muscle (skeletal); Vector: pDNR-LIB
/clontech); Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil
/ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGGGCCGACATG-dT(30)BN-3' (where B = A)
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/clone="IMAGE:4247003"
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                                                                 Holzman,T.,
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Tex: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                         1 (bases 1 to 497)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                          BQ327884
BQ327884.1 GI:20945640
EST.
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Location/Qualifiers
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                     Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Seq primer: SP6
Laboratory of Cancer Genetics
                                                                                sequence tags
                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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                                                               Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

88 c 79 g 117 t
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/db_xref="taxon:9606"
/clone="Plate=910 Col=8 Row=M"
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ncing Center
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REFERENCE
AUTHORS
TITLE
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BG714149/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG714149
BG714149.1 GI
                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consorti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=MR4&t2=MR4-RT0045-250401-009-g06&t3=2001-04-25&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 796)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                  High quality sequence stop: 677.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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602674594F1 NIH_MGC_96 Homo :
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High quality sequence stop: 37.
Location/Qualifiers
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Fax: +55-11-2707001
                                                               http://image.llnl.gov
Plate: LLAM10682 row: l column:
                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brazil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue mRNA and cDNA amplification were performed under low stringency conditions."
164 c 176 g 102 t 1 others
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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US-10-008-355-25 (1-10) x BG714149 (1-796)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                         http://image.llnl.gov
Plate: LLCM893 row: m column:
High quality sequence stop: 647.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

226 c 275 g 123 t
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/lab_host="DH10B"
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/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                 /clone="IMAGE:4054078"
/clone_lib="NIH_MGC_48"
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Query Match:

Pred. No.:

BASE COUNT

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AUTHORS TITLE JOURNAL

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US-10-008-355-25 (1-10) x BG115436
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/Clone=lib="MIH_MCC_88"
/Clone=lib="MIH_MCC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
/organ: pCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=QVl&t2=QVl-MT0166-
131100-476-b02&t3=2000-11-13&t4=1)
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/db_xref="taxon:9606"
/clone_lib="MT0166"
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                     Xenopus laevis
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Tel: 650 723 2227
Fax: 650 725 8251
Email: walbot@stanford.edu
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1 (bases 1 to 279)
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Xenopodinae; Xenopus
                                                                              African clawed frog
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/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: xhoI
/site_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
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/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
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RESULT 13
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                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 403)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schelleberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                      Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                  WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                              AA476126
403 bp mRNA linear vh17d08.rl Soares_mammary_gland_NbMMG Mus musculus IMAGE:875727 5', mRNA sequence.
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
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EST.
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Location/Qualifiers
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72 c 62 g 58 t 4 others
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/db_xref="taxon:8355"
/clone="XL155108"
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/dev_stage="stage 10.5"
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1 (bases 1 to 420)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt zd60g08.s1~Soares\_fetal\_heart\_NbHH19W~Homo~sapiens~IMAGE:} {\tt 345086~3', mRNA~sequence.}
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                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                         Unpublished (1995)
Contact: Wilson RK
                                         Seq primer: mob.REGA+ET
                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further insert Length; 389 Std Error: 0.00
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                                                                                                                                          Email: est@watson.wustl.edu
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quality sequence stop: 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptors (Pharmacia),
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:875727"
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/lab_host="DH10B"
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s (Pharmacia), digested with Not I and cloned into
I and Eco RI sites of the modified p773 vector.
vided by Dr. Minoru Ko, Wayne State Univ. Library
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                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                               MGI:1053865
Seq primer:
                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Mariania; Eutheria; Rodentia; Sciurognathi; Mariania; Ito 432)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                          5', mRNA sequence.
AW743569
AW743569.1 GI:7655383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW743569 432 bp mRNA linear EST 27-APR-2000 ur23d03.y1 Soares_mouse_NMBP Mus musculus cDNA clone IMAGE:3025157
                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                        Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
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h quality sequence stop: 404
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/db_xref="taxon:10090"
/clone="IMAGE:3025157"
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                                                                                                                                                               Location/Qualifiers
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/dev_stage="19 weeks"
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double-stranded cDNA was ligated to Eco RI adaptors
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Conservative:
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Дb

Locus AW743569

KEYWORDS VERSION

TITLE

FEATURES

BASE COUNT 125 מ (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

96 g 134 t

ORIGIN

Alignment S Pred. No.: 밁 QУ US-10-008-355-25 (1-10) x AW743569 (1-432) DB: Query Match: Percent Similarity: Best Local Similarity: Score: 352 GGTGGGTCTTCTGGATCCCCAGTATTT 378 2 GlyGlyAsnSerGlySerProValPhe 10 100.00% 88.89% 81.48% 1.04e+03 44.00 Gaps: Indels: Mismatches: Conservative:

Search completed: December 20, Job time: 1535.05 secs 2002, 15:48:51

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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79.6	/9.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	79.6	81.5	81.5	81.5	81.5	81.5	88.9	90.7	90.7	100.0	100.0	100.0	100.0	
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ALIGNMENTS

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AA015228
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis \,
                                                    WPI; 2002-490075/52.
                                                                                                                                                                                                                                                      Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; active site; DPP-7 inhibitor identification; periodontal disease; ginglvitis; periodontitis.
                                                                            Travis J,
                                                                                                                                                       08-NOV-2001; 2001WO-US46782
                                                                                                                                                                                                                      Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                       Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) active site
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                                                                                                                                                                               16-MAY-2002.
                                                                                                                                                                                                        WO200238742-A2.
                                                                                                     (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                            Potempa JS,
                                                                            Banbula A,
                                                                            Bugno
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Claim

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Page

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English

The invention comprises the amino

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AAO15206
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Best Local
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The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention au useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful reducing the growth of a bacterium and protecting an animal from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonas gingivalis dipeptidylpeptidase-7 (ppp-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents an active site region of the Porphyromonas gingivalis dipeptidase-7 (DPP-7)
                                                                           The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.
                                                                                                                                                                                           Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dipeptidylpeptidase-7; DPP-7; enzyme; DPP-7 inhibitor identification; perior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-2002
                                                                                                                                                              Example 6;
                                                                                                                                                                                                                                                                                                                          (UYGE-) UNIV GEORGIA RES FOUND INC
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periodontal disease; gingi
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                                                                                                                                                                                                                                                                                        Bugno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gingivitis
                  are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                            of
                                 are
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Qγ

1 TGGNSGSPVF

Query Match Best Local S Matches 10

Similarity

100.0%;

Score 54; Pred. No.

0.17;

DB 23;

Length

52

Conservative

0

Mismatches

0,

Indels

0;

Gaps

0

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RESULT 3
AAO15207
ID AAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                     The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Staphylococcus aureus V8 endopeptidase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-terminal region of the (DPP-7) enzyme.
                                                                                                                                                                                                                                                  Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal
                                                                                                                                                                                                                                                                                                                         Travis J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingi periodontitis; V8 endopeptidease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Porphyromonas gingivalis dipeptidylpeptidase-7
Sequence
                                                                                                                                                                                                             Example 6;
                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200238742-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO15207 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                     (UYGE-) UNIV GEORGIA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA015207
                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGGNSGSPVF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGNSGSPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                         caused
                                                                                                                                                                                                          Fig 5; 65pp;
52
                                                                                                                                                                                                                                                                                                                         Potempa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US46782
                                                                                                                                                                                                                                                                                                                                                                                 2000US-246827P
AA;
                                                                                                                                                                                                                                        Λq
                                                                                                                                                                                                                                        Porphyromonas
                                                                                                                                                                                                                                                                                                                           JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                           Banbula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                      gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                        Bugno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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TGGNSGSPVF 10

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RESULT 4
AAR91042
ID AAR9
XX AAR9
AC AAR9
DT 23-M
XX Link
KW recc
KW r
                                                                                                                                                                                             RESULT 5
AAR91043
     DEXTXACXID
                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linker peptide: V8 protease: Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli: transposon Tn903; aminoglycoside 3'-phosphotransferase.
     84
                                                         23-MAY-1996
                                                                                                               AAR91043;
                                                                                                                                                                AAR91043 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; Fig 14a; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-141021/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus strain V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V8 mature protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91042 standard; Peptide; 213 AA.
                                                                                                                                                                                                                                                                                                          165 TGGNSGSPVF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
mature protease (aal-214)
                                                                                                                                                                                                                                                                                                                                         1 TGGNSGSPVF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0296028.
94JP-0238595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95EP-0306235
                                                                                                                                                                Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (aa1-213)
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                   214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27733).
                                                                                                                                                                                                                                                                                                                                                                                                                                           0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 6
AAR91044
QУ
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                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                              A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant protein; fusion protein; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903;
                                                                                      Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                           Linker peptide; V8 protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohsuye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus strain V8 (ATCC 27733).
                                                             Staphylococcus
                                                                                                                  recombinant
                                                                                                                                                       V8 mature protease (aa1-215).
                                                                                                                                                                                                            AAR91044;
                                                                                                                                                                                                                                     AAR91044 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 14b; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP700995-A2
                                                                                                                                                                                  23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                      165 TGGNSGSPVF 174
                                                                                                                                                                                                                                                                                                                               1 TGGNSGSPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                       host cells.
                                                                                                                                                                                                                                                                                                                                                         10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                             214 AA;
                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-0296028.
94JP-0238595.
                                                             aureus strain V8 (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95EP-0306235
                                                                                                                                                                                                                                                                                                                                10
                                                                                                 in; fusion protein; beta-galactosidase;
transposon Tn903;
                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                     Score 54;
Pred. No.
                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                             27733)
                                                                                                                                                                                                                                                                                                                                                                     DB 17;
0.73;
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                   214;
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RESULT 7
AAR29644
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
          N-PSDB; AAQ27988
                                                                                                                                                                                                                      Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohsuye K,
                      WPI; 1992-304938/37
                                                                                                                                JP04211370-A.
                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                         11-FEB-1993
                                                                                                                                                                                                                                                                                                               AAR29644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1994;
07-SEP-1994;
                                                                                     19-FEB-1991;
                                                                                                           03-AUG-1992
                                                                                                                                                                                                                                            Protease;
                                                                                                                                                                                                                                                                   Protease from
                                                                                                                                                                                                                                                                                                                                   AAR29644 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Fig 14c; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-1995;
                                         (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                                                                                                                                     1 TGGNSGSPVF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host cells.
                                                                                                                                                                                                                                                                                                                                                                                          TGGNSGSPVF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
10; Conserv
                                                                                                                                                                                                                                            PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                90JP-0040398
                                                                                                                                                                                                                        aureus
                                                                                                                                                                                                                                            amplify; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0296028
94JP-0238595
                                                                                    91JP-0024633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95EP-0306235
                                                                                                                                                                 /label= Signal_peptide
69..336
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                      /label= Protease
                                                                                                                                                                                                                                                                   Aureus
                                                                                                                                                                                                                                                                                                                                    Protein; 336 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                               .74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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RESULT 8
AAR91033
     В
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Best Local Similarity
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Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pG97S4DhCT(G)R6, yielding pV8RPT(-) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAR26842 and AAR29644 are proteases which we isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                              Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                            Ohsuye K,
                                                                                                                                                                                                                              07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric Staphylococcus aureus strain V8
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                           Example 2; Page 12-13; 44pp; English.
                                                                                                                                                                                                                                                                  06-SEP-1995;
                                                                                                                                                                                                                                                                                                                  EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-galactosidase-V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91033 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 15-16;
                                                                                                                                                                                                                                                                                           13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V8 protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91033;
                                                                                                                                                                                                     (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 TGGNSGSPVF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGGNSGSPVF 10
                                                                                                                                                      1996-141021/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli;
                                                                                                                                                                              Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                              94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                                  95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                   /note= "beta-galactosidase 125..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-galactosidase;
                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease
                                                                                                                                                                                                                                                                                                                                         "mature V8 protease without the repeat region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant
Escherichia
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1.2;
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                                                                                                                                                                                                                                                                                                                                                                               region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
      The invention relates to new mutant Staphylococcus aureus V8 proteases Which have enzyme activity even under environmental conditions which promote protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 48 amino acids linked, via a synthetic linker, CC downstream of the E. coli beta-galactosidase. The S. aureus portion of the chimaera was amplified by the primers AAT73254-5 from wild type sequence. The coding sequence was then used to generate mutants of the V8 protease which retain their levels of activity in the presence of a cc higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Region
                                                                                                                                                                                                                              Claim 2; Page 13-14; 42pp; English
                                                                                                                                                                                                                                                                            Staphylococcus aureus V8 protease mutants - with
                                                                                                                                                                                                                                                                                                         WPI; 1997-013693/02
                                                                                                                                                                                                                                                                                                                                     Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by pV8RPT(-) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW22218 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pV8\text{RPT(+), respectively.} Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                              resistance to denaturation
                                                                                                                                                                                                                                                                                                                                                                  (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP745669-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteolytic activity; fusion protein; beta-galactosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              truncation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGNSGSPVF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus; V8 protease; enzyme; der ion; wild type; PCR; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                     Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             95JP-0170086
                                                                                                                                                                                                                                                                                                                                                                                                                            96EP-0303939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101..120
/note= "synthetic R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "truncated S. aureus V8 protease portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "E. coli beta-galactosidase portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
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                                                                                                                                                                                                                                                                            increased
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on; amplification;
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RESULT 11
AAR91034
ID AAR91
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AC AAR91
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AAR26842
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Best Local S
Matches 10
                                                                                                        Query Match
Best Local Similarity
Matches 10; Conser
                                                                                                                                                               The sequences given in AAR26842 and AAR29644 are proteases which were isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                        Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                Sequence
                                                                                                                                                                                                                                     Disclosure; Page 13-15;
                                                                                                                                                                                                                                                                                               WPI; 1992-304938/37.
N-PSDB; AAQ27987.
                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                            JP04211370-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR26842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR26842 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                 20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                            (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                                    19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; PCR; amplify; Staphylococcus
                                                                    233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 TGGNSGSPVF 298
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                                                                    TGGNSGSPVF 242
                                                                                     TGGNSGSPVF 10
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                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                 90JP-0040398
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                                                                                                                                                                                                                                                                                                                                                                     91JP-0024633
                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signal_peptide
69..358
                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                100.0%;
                                                                                                                                                                                                                                      25pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCC12600
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                                                                                                                Score 54;
Pred. No.
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Pred. No. 1.2;
Nismatches
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                                                                                                          Mismatches
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                                                                                                         0,
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                                                                                                                           Length 357;
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                                                                                                        Gaps
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AAR91034;

AAR91034 standard; Protein; 392 AA

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Best Local S
Matches 10
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pG97S4DhCT(G)RG, yielding pV8RPT(+), and pV8RPT(+), respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
               Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escharichia coll; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                              Recombinant V8
                                                                                                                                                                                               23-MAY-1996
                                                                                                                                                                                                                                              AAR91035
                                                                                                                                                                                                                                                                                             AAR91035 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                            TGGNSGSPVF 298
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1 Similarity 100.0%;
10; Conservative (
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protein; beta-galactosidase;
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Staphylococcus au
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                                                                                                                                                                                             (first
                                                                                                                                              protease V8D
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94JP-0238595
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125..39
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                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "mature V8 protease including the repeat region" % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus strain
                                                                                                                                                                                                                                                                                               532
                                                                                                                                            fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DE
Pred. No. 1.4
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion protein
                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V8 (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 13
AAW22219
ID AAW22
XX
AC AAW22
XX
DT 11-SE
XX
DE Prote
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                                                                                                                                                                                                   В
                                                                                                                                                          Best Local Similarity Matches 10; Conserv
                                                                                                                                                                              Query Match
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Chimeric
Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                             Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Region
                                                                                                                                                                                                                              respectively), B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker peptide (AAR91032). The fusion protein is expressed in inactive form in E coli. It is then recovered, solubilised and cleaved at the linker peptide regions with a protease intrinsic to the host cells, i.e.
                                                                                                                                                                                                                                                                                A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides (derived from Escherichia coli beta-galactosidase and and Tn903 aminoglycoside 3'_phosphotransferase,
                                                              AAW22219 standard; Protein;
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                        Example 3; Page 16-18; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                            Ohsuye K, Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-1994;
07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                (SUNR)
                                                                                                                  289 TGGNSGSPVF 298
                                                                                                                                      L
                                                                                                                                      TGGNSGSPVF 10
                                                                                                                                                                                                                      protease, to allow
                                                                                                                                                                                                                                                                                                                                                                                                                                SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic;
Staphylococcus aureus strain
transposon Tn903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli;
                                                                                                                                                                                                   532 AA;
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    94JP-0296028.
94JP-0238595.
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339..340
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101..1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "R6 linker'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "aminoglycoside 3'phosphotransferase
region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "R6 linker"
                                                                                                                                                                                                                     recovery of V8
                                                                                                                                                                              .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protease
                                                               532
                                                                                                                                                          0;
                                                                                                                                                         Score 54; DB 1
Pred. No. 1.9;
0; Mismatches
                                                               AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for OmpT
                                                                                                                                                                                                                      protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region'
                                                                                                                                                                             17;
                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease"
                                                                                                                                                                             Length 532;
                                                                                                                                                          Indels
                                                                                                                                                          0
                                                                                                                                                                                                                                                     in E.
                                                                                                                                                          Gaps
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Protein encoded by pV8D construct.

11-SEP-1997

(first entry)

0

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RESULT 14
AAW22220
                                                                                                                                                                                                                                                                                                                                                                                                    CC The invention relates to new mutant Staphylococcus aureus V8 proteases CC which have enzyme activity even under environmental conditions which CC promete protein denaturation. The mutants are based on 3 truncated V8 CC proteases lacking 48 (AAW22218), of 56 (AAW22219) or 53 (AAW22220) amino CC contain amino acid substitutions, especially D44E, N715 and/or R147K. CC The protein sequence shown here represents a chimaeric protein CC comprising a truncated Staphylococcus aureus V8 protease lacking the CC prepro and C-terminal 56 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the Protease fragment is a second R6 linker and a fragment of the CC aminoglucoside 3'-phosphotransferase protein. The chimaeric sequence CC was generated by restriction digestion and ligation from the VRPT(-) CC sequence (see AAW22218) by using a natural EcoRV site which removed a CC further 8 amino acid from the C-terminus. This truncated V8 protease, cold designated V8D, retains its level of activity in the presence of a cc higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric
Chimeric
AAW22220;
                                         AAW22220 standard; Protein; 537 AA.
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus V8 protease mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-013693/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohsuye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification; proteolytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                         289
                                                                                                                                                                                                                                                                   Local Similarity
les 10; Conserv
                                                                                                                                                                                                                     1 TGGNSGSPVF 10
                                                                                                                                                                       TGGNSGSPVF 298
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                                                                                                                                                                                                                                                                                                                                                                  532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
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                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  denaturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95JP-0170086
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125..336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "R6 linker sequence"
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                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                        Score 54; DB Pred. No. 1.9;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                            Length 532;
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RESULT 15

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                                                             Matches
                                                                           Query Match
Best Local :
                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus V8 protease mutants - with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-013693/02
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 289
                                                           Local Similarity
nes 10; Conser
                              1 TGGNSGSPVF 10
TGGNSGSPVF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded by pV8F construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to denaturation
                                                          100.
nilarity 100.
Conservative
                                                                                                                         537 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
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101..124
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                                                                          Score 54; DB
Pred. No. 1.9;
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                                                                                                                                                                                                                            The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase 7 (DPP-7) enzyme. The DP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 4; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
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DB; AAL43635.
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ilarity 100.0%;
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RESULT 1 PRSASK

glutamyl endopeptidase (EC 3.4.21.19) precursor - Staphylococcus aureus N;Alternate names: staphylococcus serine proteinase C;Species: Staphylococcus aureus C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999 C;Accession: A26812; A00966 R;Carmona, C: Gray, G.L. Nucleic Acids Res. 15, 6757, 1987 Nucleic Acids Res. 15, 6757, 1987 A;Title: Nucleotide sequence of the serine protease gene of Staphylococcus aureus, A;Reference number: A26812; MUID:87316953; PMID:3306605 A;Accession: A26812

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RESULT 2
G89873
hypothetical protein sspA [imported] - Staphylococcc.
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Accession: G89873
R;Suroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Cac, Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Tancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain V8
C;Comment: This extracellular proteolytic enzyme preferentially cleaves the peptide b C;Comment: This extracellular proteolytic enzyme preferentially cleaves the peptide b C;Comment: This enzyme may be distantly related to the trypsin-type serine proteinase dues.
C;Superfamily: staphylococcal serine proteinase
C;Keywords: hydrolase; serine proteinase
F;69-336/Product: staphylococcal serine proteinase #status experimental <ACT>
F;119,161/Active site: His, Asp #status predicted
F;237/Active site: Ser #status experimental
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A;Tit.Le: The primary structure of staphylococcal protease
A;Reference number: A23824; MUID:78212487; PMID:96922
A;Accession: A00966
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A; Residues: 69-108; 110-124; 126-144, 'D', 146-192, 'T', 194-228, 'N', 230-258, 'Q', 260, 'D', 26
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A; Residues: 1-336 <CAR>
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
                                                                                                                                                                                                           A:Molecule type: DNA
A:Residues: 1-716 <SIM>
A:Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSPDB:GN00:
A:Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                                   A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA A;Residues: 1-357 <YOS>
A;Cross references: GB:D00730; NID:g216970; PIDN:BAA00630.1; PID:g216971 C;Superfamily: staphylococcal serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;YOshikawa, K.; Tsuzuki, H.; Fujiwara, T.; Nakamura, E.; Iwamoto, H.; Matsumoto, K.; S: Biochim. Biophys. Acta 1121, 221-228, 1992
A;Title: Purification, characterization and gene cloning of a novel glutamic acid-speci A;Reference number: S21758; MUID:92287954; PMID:1599945
A;Accession: S21758
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutamic acid-specific endopeptidase - Staphylococo
(;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
C;Accession: S21758
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C;Superfamily:
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A:Cross references: GB:BA000018; PID:g13700850; A:Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                      R; anonymous, The Xylella fastidiosa Consortium Nature 406, 151-157, 2000\,
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                          Query Match
Best Local
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       Matches
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A; Molecule type: protein A; Residues: 95-316 <SVE>C; Keywords: hydrolase
                                                                                 A; Reference number: S23078;
A; Accession: S23078
                                                                                                                         A; Title: Isolation and amino acid
                                                                                                                                                            R; Svendsen,
                                                                                                                                                              A;Note: sequence extracted from NCBI backbone (NCBIN:118784, R;Svendsen, I.; Breddam, K.
                                                                                                                                                                                                      A;Cross-references: GB:D10060; NID:g216263; PIDN:BAA00949.1; A;Experimental source: ATCC 14580
                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <KAK>
                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 267, 23782-23788, 1992
A;Title: Purification, Characterization, cloning, and expression A;Reference number: A45134; MUID:93054737; PMID:1429718
A;Accession: A45134
                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A45134; S23078
                                                                                                                                                                                                                                                                                                                                                                                                                         endopeptidase (EC 3.4.-.-), glutamate-specific - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z12296; NID:g43337; PIC:Superfamily: staphylococcal serine proteinase
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A; Residues: 1-284 <SUY>
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A;Accession: S25140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S25140
R;Su, Y.A.; Clewell, D.B.
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C; Date: 20-Feb-1995 #sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodrigues, V.; Rosa, A.J. de M.;
A;Authors: da Silva, A.C.R.; da (
M.; Tsuhako, M.H.; Vallada, H.; V
A;Reference number: A59328
                                                          A;Status: preliminary
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Best Local S
Matches 9
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                                                                                                                                              J. Biochem. 204, 165-171, 1992
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Chem. 267, 23782-23788, 1992
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9; Conserv
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70.0%;
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                                                                                                    o acid sequence
MUID:92155199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; de Rosa Jr., V.E.; de Sa, R.G.; Santell
Silva, F.R.; da Silva, A.M.; Silva Jr.,
Van Sluys, M.A.; Verjovski-Almeida, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,.
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Pred. No.
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                      K.; Fujiwara, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-Feb-1995
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of gelE
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2.8;
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                                                                                                                         acid
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                                                                                                                                                                                                                           PID:d1001415;
                                                                                                                                                                                 NCBIP:118785)
                                                                                                                         specific endopeptidase
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lva Jr., W.A.; da
ida, S.; Vettore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          faecalis
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Similarity 8; Conser

Conservative

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88

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Score 43; DB Pred. No. 8.5; 0; Mismatches

DВ 3.5;

2

Length 316;

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Gaps

0

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A; Molecule type: DNA
A; Residues: 1-50 < HTL>
A; Cross-references: EBBL: U43738
R; Himmelreich, R; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A; Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneu A; Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneu A; Reference number: S73327; MUID:97105885; PMID:8948633
A; Accession: S73576
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-521 (HIZ)
A; Cross-references: EMBL:AE000025; GB:U00089; NID:g1673918; PIDN:AAB95898.1; PID:gA; C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
SGC3
C; Superfamily: hypothetical protein MG068
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C; Accession: AI2436
C; Accession: AI2436
C; Accession: AI2436
                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: EMBL:U43738; NID:g1209757; PIDN:AAC43664.1; PID:g1209771 R;Hilbert, H.; Himmelreich, R.; Plagens, H.; Herrmann, R. Nucleic Acids Res. 24, 628-639, 196 A;Title: Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma A;Reference number: S62797; MUID:96177562; PMID:8604303 A;Accession: S62798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change
C;Accession: S62794; S62798; S73576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:BA000019;
A;Experimental source: strain PC
C;Genetics:
A;Gene: alr5049
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2436
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AI2436
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A; Molecule type: DNA
A; Residues: 1-521 <HIM>
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N;Alternate names; MG395 homolog D02_orf521
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                                                                                   EMBL:AE000025; GB:U00089; NID:g1673918; PIDN:AAB95898.1; PID:g16739:
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88
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C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 *sequence_revision 19-Oct-1995 *text
C;Accession: A56940
R;Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama, K.
J. Biol. Chem. 270, 14471-14476, 1995
A;Title: Strain-specific presence of two TGN38 isoforms A;Reference number: A56940; MUID:95301533; PMID:7540170
A;Accession: A56940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama, J. Biol. Chem. 270, 14471-14476, 1995
A;Tille: Strain-specific presence of two TGN38 isofo A;Reference number: A56940; MUID:95301533; PMID:7540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
C;Accession: B56940
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C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Date: 21-729
C;Accession: E71729
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: C; Genetics: A; Gene: htrA; RP186
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-361 <KAS>
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A;Experimental source: strain Madrid E
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A; Residues: 1-315 < AND>
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                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references:
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                                                                                                                                                            integral membrane protein TGN38B - mouse
                                                                                                                                                                                A56940
                                                                                                                                                                                                   RESULT 11
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A71630; MUID:99039499;
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87.5%;
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88.9%;
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77.88;
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Pred. No.
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31;
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                                         mouse
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C;Genetics:
A;Gene: RC02
C;Keywords:
RESULT 14
JN0453
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173898; PMID:11259647
A;Accession: E87365
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
""" 7; Conserv
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A; Molecule
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A:Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97729
A;Status: prellminary
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A; Residues: 1-497 <KUR>
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7; Conservative
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88.9%;
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87.5%;
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Pred. No.
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Pred. No.
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43;
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C;Accession: AE3453
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dihydroorotate oxidase (EC 1.3.3.1) - gill mushroom (Agrocybe aegerita) R;Alternate names: dihydroorotate dehydrogenase C:Species: Agrocybe aegerita C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-C;Accession: JN0453
Search completed: December Job time: 34.8421 secs
                                                                                     Вр
                                                                                                                            δÃ
                                                                                                                                                                                                                                                               C; Keywords:
                                                                                                                                                                                                                                                                             A; Map position: I
C; Superfamily: dihydroorotate oxidase
                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-364 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52792.1; PID:917983628; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dihydroorotate oxidase (EC 1.3.3.1) [imported] - Brucella melitensis (strain C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 122, 233-234, 1992
A;TITL1e: Sequence of the URA1 gene encoding dihydroorotate dehydrogenase from the bas
A;Reference number: JN0453; MUID:93083991; PMID:1452035
A;Accession: JN0453
                                                                                                                                                                                                                                                                                                                              A; Gene: BMEI1611
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A; Residues: 1-328 < NOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Noeel, T.; Labarere, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: URA1
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Best Local Similarity
Matches 7; Conserv
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                    20,
                    2002,
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Pred. No.
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Maximum DB
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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      2002, 11:25:03; Search time 12.6316 Seconds
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    US-10-008-355-25
US-10-008-355-4
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US-10-008-355-7
US-09-815-242-12277
US-09-815-242-12277
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US-09-388-089B-12
US-09-388-089B-12
US-09-388-089B-12
US-09-388-089B-11
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13.271 Million cell updates/sec
Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1834, A
Sequence 1277, A
Sequence 12277, A
Sequence 12, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 35385, A
Sequence 8, Appli
Sequence 2, Appli
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Sequence 3, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 26, Appli
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ALIGNMENTS

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; OTHER INFORMATION: Consensus sequence US-10-008-355-25
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US-10-008-355-25
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Sequence 3, Application US/10008355
Patent No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 25
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Patent No. US20020164759A1
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Best Local :
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10
                                                                                                                                                                                                                                                                                                           Local Similarity
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FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08

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PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILLING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 52
TYPE: PRT
ORGANISM: Porphyromonas gingivalis
US-10-008-355-3
                                                                                    Sequence 8, Application US/10008355

Patent No. US20020164759A1

GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agniesaka
APPLICANT: Banbula, Agniesaka
FILE REFERENCE: 235.00440101

CURRENT APPLICATION NUMBER: US/10/008,355

CURRENT FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: US 60/246,827

PRIOR FILING DATE: 2000-11-08

NUMBER OF SEQ ID NOS: 26
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US-10-008-355-8
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TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-008-355-4
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 8 LENGTH: 699
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Patent No. US20020164759A1
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CORRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0
ORGANISM: Porphyromonas gingivalis
                     TYPE: PRT
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Pred. No. 0.012;
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Pred. No. 0.012;
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Qy
                                                                                                                                      : SOFTWARE: PatentIn version 3.0

: SEQ ID NO 6

: LENGTH: 732

: TYPE: PRT

: ORGANISM: Shewanella putrefaciens

US-10-008-355-6
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US-10-008-355-2
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LENGTH: 712
TYPE: PRT
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Matches
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10008355 Patent No. US20020164759A1
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Best Local Similarity
Matches 10; Conserv
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                                                                                                     Query Match
                                                                                                                                                                                                                                            APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235,00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/246,827 PRIOR FILING DATE: 2000-11-08 NUMBER OF SEQ ID NOS: 26
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662 TGGNSGSPVF 671
                                                                  Local Similarity hes 10; Conserv
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                                 1 TGGNSGSPVF 10
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                                                                   Conservative
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                                                                                    100.0%; Score 54; DB 9; 100.0%; Pred. No. 0.17;
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Pred. No. 0.17;
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Pred. No. 0.17;
                                                                   Mismatches
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US-10-008-355-26

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Query Match
Best Local Similarity
"atches 9; Conserva
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Best Local Similarity
""" 9; Conserv:
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US-10-008-355-9
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TYPE; PRT
; ORGANISM: Xylella fastidiosa
US-10-008-355-7
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                                                                                    GENERAL INFORMATION:
                                                                                                    Sequence 9, Application US/10008355
Patent No. US20020164759A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235,00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR APPLICATION SUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEO ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
                           APPLICANT: Travis, James
APPLICANT: Potempa, Jan
APPLICANT: Banbula, Agn
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%; Pred. No. 1.6
0; Mismatches
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Pred. No.
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; LENGTH: 734
TYPE: PRT
: ORGANISM: Shewanella putrefaciens
US-10-008-355-5
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US-09-864-761-48349
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; LENGTH: 720
; TYPE: PRT
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/246,827 PRIOR FILING DATE: 2000-11-08 NUMBER OF SEQ ID NOS: 26
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Travis, James APPLICANT: Potempa, Jan APPLICANT: Banbula, Agn
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CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665 TGGNSGSP 672
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APPLICATION NUMBER:

2000-10-04 NUMBER: US 2000-09-27

us 60/236,359

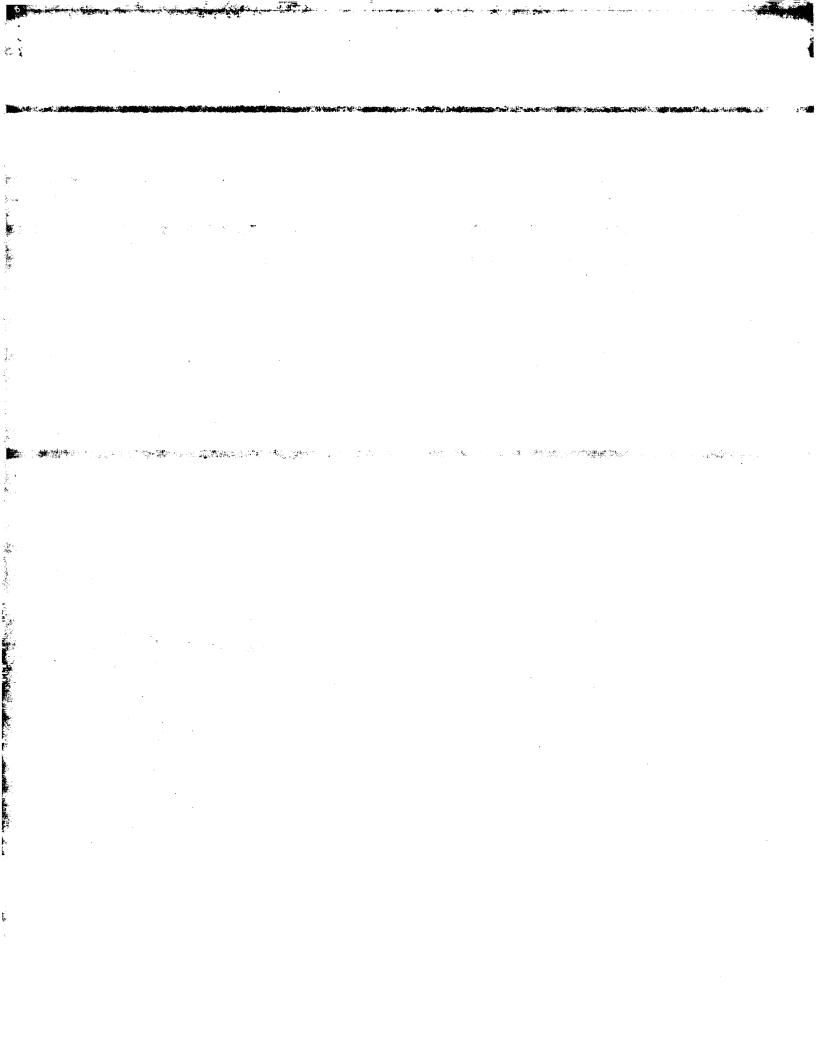
NUMBER: GB 24263.6

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; OTHER INFORMATION: MAP TO AL121716.16
; OTHER INFORMATION: EXPRESSED IN LUNC, SIGNAL = 1.9
; OTHER INFORMATION: EST_HUMAN HIT: BE002805.1, EVALUE 8.00e-39
; OTHER INFORMATION: SWISSPROT HIT: Q9ZKD2, EVALUE 3.60e+00
US-09-864-761-48349
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US-09-815-242-5351
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 48349
                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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nes 6; Conserv
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APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                            INFORMATION:
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Trawick, John D.
Carr, Grant J.
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; ORGANISM: Staphylococcus aureus US-09-815-242-5351
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR APPLICATION NUMBER: 60/243,578
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SEQ ID NO 5351
LENGTH: 240
TYPE: PRT
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SOFTWARE: FastSEQ for
SEQ ID NO 12277
LENGTH: 254
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FILING DATE: 2000-12-22
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Trawick, John D.
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Zyskind, Judith W.
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Sequence 2, Application US/09388089B
Patent No. US20020018782A1
GENERAL INFORMATION:
APPLICANT: Jackson, W.
APPLICANT: Jackson, W.
APPLICANT: HATRIS, A.
TITLE OF INVENTION: NEISSERIA MENINGITIDIS POLYPEPTIDE, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-083
CURRENT FILING DATE: 1999-08-31
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 447
TYPE: PRT
ORGANISM: Neisseria spp.
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/388,089B
COURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 20
SOTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 475
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-388-089B-12
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Best Local Similarity
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US-09-388-089B-12
; Sequence 12, Application US/09388089B
; Patent No. US20020018782A1
Search completed: December 20, 2002, 12:17:26 Job time: 13.6316 secs
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US-09-388-089B-2
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APPLICANT: Jackson, W.
APPLICANT: Harris, A.
TITLE OF INVENTION: NEISSERIA MENINGITIDIS POLYPEPTIDE, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-083
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Best Local Similarity 75.0
Matches 6; Conservative
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EMBL; Y00356; CAA68434.1; -. EMBL; AF309515; AAG45843.1;

PIR; A26812; PRSASK. MEROPS; S01.269; -.

IPR000126; Ser_proteas_V8

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Eur. J. Biochem. 204:165-171(1992)
-i- FUNCTION: SPECIFIC FOR HYDROLYSIS OF PEPTIDES BONDS ON THE CARBOXYL SIDE OF ACIDIC AMINO ACID RESIDUES, WITH A STRONG PREFERENCE FOR GLU.

PREFERENCE FOR GLU.
-i- CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-xaa, Glu-|-xaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSEP_BACLI
P80057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequer 16-OCT-2001 (Rel. 40, Last annota Glutamyl endopeptidase precursor
                                                between
                                                                                                                                                                                      Svendsen I.,
                                                                                                                                                                                                MEDLINE-92155199;
                                                                                                                                                                                                             SEQUENCE OF 95-316.
                                                                                                                                                                                                                                                      Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E., Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N.; "Purification, characterization, cloning, and expression of a glutamic acid-specific protease from Bacillus licheniformis ATCC
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-ATCC 14580; MEDLINE-93054737; PubMed-1429718;
                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                          Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                endopeptidase) (GSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0839; V8PROTEASE.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                               14580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 TGGNSGSPVF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGGNSGSPVF 10
            ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for con
                                                                                SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B.
                                                SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease;
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2599
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                                                                                                                                                                                                                                  267:23782-23788(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                 PubMed=1346764;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
MISSING (IN REF. 3).
MISSING (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 1;
Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8B138D0C7996AA3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          ation update) (EC 3.4.21.19)
                                                                                                                                                                                                                                                                                                                                                              Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 336;
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            is in no way for commercial
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PRRRAPE REPRESENTATION OF THE PRESENTATION OF 
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Best Local S
Matches 8
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076062; 095982; Q96GZ1; Q96E64;

15-UUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
(Sterol C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily member 2) (Another new gene 1) (Putative sterol reductase SR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10060;
PIR; S23078; S
PIR; A45134; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
ACT_SITE
ACT_SITE
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                          MEDLINE-99097347; PubMed-9878250; MEDLINE-99097347. Morman H.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00839; VBPROTEASE.
SMART; SM00020; TIYP_SPC; 1.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
                                                                                                                                                                         Strausberg R.;
Submitted (MAY-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98277456; PubMed=9615229;
Lemmens I.H., Kas K., Merregaert J., Van De Ver
"Identification and molecular characterization
gene cluster on human chromosome 11q13.";
Genomics 49:437-442(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _HUMAN
                                                                 Roberti R.,
Beccari T.,
                                                                                                                                                                                                                                                                                   Genomics
                                                                                                                                                                                                                                                                                                     Holmer L., Pezhman A., Worman H.J.; "The human lamin B receptor/sterol reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        member 2) (Another new TM7SF2 OR ANG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000126; Ser_proteas_V8.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                      Roberti R., Bennati A.M.,
Beccari T., Della Fazia M
"Cloning and expression o
                                                                                                            PubMed=11784322;
                                                                                                                                FUNCTION
                                                                                                                                                                                                                      TISSUE=Brain, and
                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                      Liver
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A45134; A45134.
  Biochem.
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8; Conser
                                                                                                                                                                                                                                                                                   54:469-476(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAA00949.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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9; V8PROTEASE.
269:283-290(2002)
                                                                                                                                                                                                                  Eye;
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141
261
142
279
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94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33611
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88.9%;
                                        M.A., Servillo G.;
of sterol Deltal4-reductase
                                                                                                                                                                           the
                                                                                 Galli G.,
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POTENTIAL
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); Mismatches
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CHARGE RELAY SYSTEM (B)
CHARGE RELAY SYSTEM (B)
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(BY
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SIMILARITY).
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RESULT 4
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Best Local Similarity
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>:</del> :
SEQUENCE FROM N.A. STRAIN-ATCC 29342 MEDLINE-96177562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM TRANSMEM
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                                                                                                                                       MPN592
                                                                                                                                                     Hypothetical lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                            NCBI_TaxID=2104;
                                                                                                  Bacteria;
                                                                                                                  Mycoplasma
                                                                                                                                                                         16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                               16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEN
                                                                                                                                                                                                                                                                                                                                                    163 GGNSGNPIY 171
                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Executive Buropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Expressed in adult heart, brain, portions, liver, skeletal muscle, kidney, ovary, prostate, lung, liver, skeletal muscle, kidney, liver, skeletal muscle, kidney, liver, live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION:
CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: Ref.1 sequence differs from that sequencing problems as reported in Ref.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             but not detected in placenta, spleen, thymus, small intestine, colon (mucosal lining), or peripheral blood leukocytes. SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-ol + NADPH
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AF023676; AAC21450.1; ALT_FRAME.
AF09303; AAD09765.1; -.
AF096304; AAD09765.1; -.
BC019852; AAH09052.1; -.
BC012857; AAH12857.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:11863; TM7SF2
                                                                                                                                       OR MP250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01222; ERG4_ERG24; 1.
PS01017; STEROL_REDUCT_1;
PS01018; STEROL_REDUCT_2;
                                                                                              a pneumoniae.
Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001171; ERG4_ERG24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reticulum;
13 81
62 124
102 124
129 148
255 277
285 377
285 377
299 299
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                                                                                                                                                                       (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                           1:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                      STANDARD;
/ M129;
PubMed=8604303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46417 MW;
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                                                                                              Mollicutes;
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Pred. No.
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POTENTIAL.
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POTENTIAL.
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L -> V (IN REF. 3
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                                                                                                                                                     precursor (DC
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                              Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from that shown due
                                                                                                                                                                                                                                                      521 AA
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CRC64;
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prostate, and testis,
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Best Local
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                                                                                                                                                                                                                                               PYRD_AGRAE
P28294;
01-DEC-1992
                                                                                                                                                                                                                                                                                       AGRAE
                                                                                                                                                                                                         01-DEC 1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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SEQUENCE FROM N.A.
M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
-!- COFACTOR: FAD.
-!- PATHWAY: Pyrimidine biosynthesis; fourth step.
                                       "Sequence of the URA1 gene encoding the basidiomycete fungus Agrocybe ae Gene 122:233-234(1992).
-i- CATALYTIC ACTIVITY: (S)-dihydroc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U43738; AAC43664.1; -. EMBL; AE000025; AAB95898.1; -.
                                                                                                  SEQUENCE FROM N.A. MEDLINE=93083991; PubMed=1452035;
                                                                                                                                                  Eukaryota; Fungi; Basidion Agaricales; Bolbitiaceae;
                                                                                                                                                                                         URA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00840; Y06768FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002414; DUF30/31. Pfam; PF01727; DUF30; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Himmelreich R., Hilbert H.,
                                                                                         Noel T., Labarere J
                                                                                                                                                                            Agrocybe aegerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE MG067 / MG068 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97105885;
                                                                                                                                                                                                 (DHOdehase)
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                H(2)O(2).
COFACTOR: FAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                       521 AA;
                                                                                                                                                                                                   (DHODase) (DHOD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Lipoprotein;
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                                                                                                                                                                                                                                                                          STANDARD;
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521
23
59500 ,
                                                                                                                                                               Basidiomycota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                 75.9%;
77.8%;
                                        (S)-dihydroorotate
                                                                 Agrocybe aegerita
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N-ACYL DIGLYCERIDE (POTENTIAL).
; 0E706CDEC8CEEBDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                               Hymenomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 521;
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                                                                                                                                                               Homobasidiomycetes;
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                                                                            dehydrogenase
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MBL outstation -
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Best Local S
Matches 7
InterPro; IPRO02022; Amb_allergen.
Pfam; PF00544; pec_lyase; 1.
Lyase; Signal; Glycoprotein; Multi-
SIGNAL 20 OR 21
CHAIN 21 378 PECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998
15-JUL-1998
15-DEC-1998
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pir; JN0453; JN0453.
InterPro: IPR001295; DHO_dh.
pfam; PF01180; DHOdehase; 1.
TIGRFAMS; TIGR01036; pyrD_sub2; 1.
                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See )
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PROSITE; PS00912; DHODEHASE_2; 1.

PyrImidine biosynthesis; Oxidoreductase; Flavoprotein; FAD.

NP_BIND 288 296 FAD (NAD PART) (POTENTIAL).

SEQUENCE 328 AA; 35085 MW; 71FA3D2A4D57EF75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                          EMBL; X65552; CAA46521.1; -. EMBL; A12248; CAA01023.1; -. HSSP; Q01172; 1IDJ.
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92357005; PubMed-1495474;
Kusters-Van Someren M., Flipphi M., de Graaff L.,
Kester H., Hinnen A., Visser J.;
"Characterization of the Aspergillus niger pelB ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus niger.
Eukaryota; Fungi;
Eurotiales; Tricho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                               regulation of expression.";
Mol. Gen. Genet. 234:113-120(1992).
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                                                                                                                                         or send
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5061;
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                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Eliminative cleavage
                                                                                                                                                                                                                                                                enuronosyl groups.
SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Eliminative cleavage of pectin to give oligosaccharides with terminal 4-deoxy-6-methyl-alpha-D-galact-4-
                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Electric the Swiss Institute of Bioinformatics and the Electric through
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                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                              Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                             120.49 / N400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 37, Last annotation update)
B precursor (EC 4.2.2.10) (PLB).
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                Multigene family OR 21 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                            niger pelB gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378
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There are no restrictions
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CARBOHYD
CARBOHYD
SEQUENCE
                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 44, Last annotation update)
Hypothetical 110.9 kDa protein in SPC98-TOM70
YNL123W OR N1897.
                                                                                                            YNM3_YEAST
P53920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V66K_BWYVF
P09506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _BWYVF
                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-MAR-1989 (Rel. 10, Last seg
01-OCT-1989 (Rel. 12, Last ann
Saccharomycetales; NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                   InterPro; IPR000382; Luteo_ORF2; Pfam; PF02122; Luteo_ORF2; 1. PRINTS; PR00913; LVIRUSORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=89057523; PubMed=3194229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae; Polerovirus.
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                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jonard
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                                                                                                                                                                                        354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of beet western yellows virus RNA.";
Nucleic Acids Res. 16:9917-9932(1988).
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                                                                                                                                                                                                                2 GGNSGSPVF 10
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             Saccharomycetaceae;
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Pred. No.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; 4FF321AF2B0B72FF CRC64;
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13;
             Saccharomyces
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Matches 7
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P09507;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative RNA-directed RNA polymerase (EC 2.7.7.48) (ORF 3).
Beet western yellows virus (isolate FL-1) (BMYV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001478; PDZ.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"The DNA sequence of cosmid 14-13b from chromosome XIV of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                         Submitted (APR-2002) to -!- CATALYTIC ACTIVITY:
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EMBL; 271399;
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[2]
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                                                                                                                                                      Jonard G.;
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                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                        Nucleotide sequence of beet western yellows Nucleic Acids Res. 16:9917-9932(1988).
                                                                                                                                                                                                                                      Jonard G
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                                                                    AND PARTIAL SIMILARITY TO SOU RNA-DEPENDENT RNA POLYMERASE.
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N nucleoside triphosphate = N di
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                                                                                 SOUTHERN BEAN MOSAIC VIRUS PUTATIVE
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                                                                                                                                                                                                                      virus RNA.";
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                           NP_BIND
SEQUENCE
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TRANSIT
                                                                                                                                                               EMBL; x62909; CAA44695.1; -.
PIR; S23762; S23762.
InterPro; IPR001295; DHO_dh.
InterPro; IPR003009; FMN_enzyme.
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93272056; PubMed=1303803;
Minet M., Dufour M.E., Lacroute F.;
"Complementation of Saccharomyces cerevisiae auxotrophic mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eddioctyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X13063; CAA31464.2; -.
PIR; S01940; RRVQFL.
InterPro; IPR001795; Luteo_RNA_pol.
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                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana cDNAs.";
Plant J. 2:417-422(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                       CHAIN
                                                                                            PYrimidine biosynthesis; Oxidoreductase; Flavoprotein; FAD:
                                                                                                                         TIGRFAMs; TIGR01036; pyrD_sub2; 1.
PROSITE; PS00911; DHODEHASE_1; 1.
                                                                                                                                                     Pfam; PF01180; DHOdehase; 1.
                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Pyrimidine biosynthesis; fourth step.
                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: FAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Dihydroorotate oxidase) (DHOdehase).
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                                                                               peptide: Mitochondrion.
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434
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                             AA;
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                          45568 MW;
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77.8%;
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 70.48;
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                                          FAD
Score 38;
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                                        DIHYDROOROTATE DEHYDROGENASE FAD (NAD PART) (POTENTIAL).
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                                                                  MITOCHONDRION (POTENTIAL)
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                           186BA05F3EF49D91 CRC64;
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1;
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HME1_MOUSE
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Matches
                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=93185339; PubMed=1363401;

Logan C., Hanks M.C., Noble-Topham S., Nallainathan D.,

Provart N.J., Joyner A.L.;

"Cloning and sequence comparison of the mouse, human, and chicken

"cloning and sequence potential functional domains and regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Last sequence upd 15-JUN-2002 (Rel. 41, Last annotation u Homeobox protein engrailed-1 (Mo-En-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HME1
                                                                                                                                                                                                                                                                                          homology to the Dros
Cell 43:29-37(1985).
[4]
                                                                                                                                                                                                                                                                                                                                                                         Joyner A.L., Martin G.R.; "En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrailed gene: expression during embryogenesis."; Genes Dev. 1:29-38(1987).
                                                                                EMBL; L12703; AAA03660.2; EMBL; Y00201; CAA68361.1;
                                                                                                                                                                                                                                        evolution.
                                                                                                                                                                                                                                                 Holland P.W.H., Williams N.A.; "Conservation of engrailed-like
                                                                                                                                                                                                                                                                                                                      Joyner A.L., Kornberg T., Coleman K.G., Cox "Expression during embryogenesis of a mouse
                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 298-401 FROM N.A. MEDLINE=86079501; PubMed=2416459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P09065
                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      MEDLINE=91099509; PubMed=1980115;
                                                                                                                                                                                                                                                                               SEQUENCE OF 321-380 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions."
                     RANSFAC;
                                                                                                                                                                                                                               FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88112776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366
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                            1; A26629; A26629.
1; A24778; A24778.
1; S13009; S13009.
1; A48423; A48423.
1; P02836; 3HDD.
                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE ENGRAILED HOMEOBOX FAMILY. SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse)
         SFAC; T02016;
MGI:95389; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGLSGKPLF 375
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7; Conservative
                                                                                                                                                                                                                                                                                                              to the Drosophila
15389; En1.
IPR000747;
                                                                                                                                                                                                                            277:250-252(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                            278-401 FROM N.A.
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Engrailed
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annotation update)
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                 homeobox sequences
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RESULT 12
CEL1_AGAB:
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Best Local S
Matches 6
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Q00023;
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SEQUENCE
    InterPro;
InterPro;
                                                                                                                                                                                                                                                          Armesilla A.L., Thurston C.F., Yaguee E.;
"CELI: a novel cellulose binding protein secreted by Agaricus bisporus during growth on crystalline cellulose.";
FEMS Microbiol. Lett. 116:293-299(1994).
-!- FUNCTION: PROBABLE GLYCOSYL HYDROLASE ACTIVE ON CELLULOSE.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBLERITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
-!- SIMILARITY: BELONGS TO FAMILY 61 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene
                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homeobox; DNA-binding; Developmental I DOMAIN 52 87 PRO-RICH DOMAIN 73 87 POLY-PRO DOMAIN 207 228 POLY-ALA DOMAIN 207 228 POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00033; ENGRALLED; 1.
                                           EMBL; M86356; HSSP; P00725;
                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-D649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agaricus bisporus (Common mushroom).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Agaricales; Agaricaceae; Agaricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellulose-growth-specific
                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raguz S., Yaguee E., Wood D.A., Thurston C.F.;
"Isolation and characterization of a cellulose-growth-specific gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046;
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                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agaricus bisporus.";
119:183-190(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGNSGSP
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IPR000254; CBD_fungal.
IPR005103; Glyco_hydro_61
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401 /
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                                                                AAA53434.1;
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35, Last sequence update)
41, Last annotation update)
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228
371
40950
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75.0%;
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POLY-ALA.
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Pfam; PF00734; CBM_1; 1. Pfam; PF03443; Glyco_hydro_61; 1.

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RESULT 13
PLYA_COLGL
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Matches
Query Match
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Matches 6; Conserv
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DISULFID
CARBOHYD
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15-DEC-1998
15-DEC-1998
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DOMAIN
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CHAIN
                                             SEQUENCE
                                                                             Pfam; PF00544; pec_lyase; 1.
Lyase; Signal; Glycoprotein.
SIGNAL 1 20
                                                                                                                                                  entities requires a or send an email to
                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                            "The pectin lyase-encoding gene (pnl cingulata: characterization of pnlA Gene 142:141-146(1994)
-i- CATALYTIC ACTIVITY: Eliminative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLYA_COLGL
Q00374;
                                                                                                                          EMBL; L22857; AAA21817.1; HSSP; Q01172; 1IDJ.
                                                                                                                                                                                                                                                                                                                                          Templeton M.D.,
Rikkerink E.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota;
Sordariomycetes incertae sedi:
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                                                                                                              InterPro; IPR002022; Amb_allergen
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SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE
                                                                                                                                                                                                                                                                        enuronosyl groups.
                                                                                                                                                                                                                                                                                  oligosaccharides with
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                                                                                                                                                          an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conser
                                          130
380
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                             AA;
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            66.7%;
60.0%;
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POTENTIAL.
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n of pnlA and its expres
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  2;
           Score 36;
Pred. No.
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Pred.
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                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
; 3DF9A99FBB482053 CRC64;
                                                                  PECTIN LYASE
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLULOSE-BINDING
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                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                   Bowen J.K., Crowhurst R.N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LINKED (GLCNAC. . 60E2C8080895CA2B
                                                                                                                                                                                                                                                                                                                                                                                                                    Phyllachorales; Phyllachoraceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
  Mismatches
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                                                                                                                                                                                                                                                                             e cleavage of pectin to give
4-deoxy-6-methyl-alpha-D-galact-4-
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36;
                       DВ
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RESULT 14
Y350_HAEIN
 Query Match
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Matches 7
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01-MAR-1992
01-NOV-1995
15-JUN-2002
                                                                          VARIANT
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REDINE-95356630, PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical HI0350.
                                                                                                                                                                                                                             PIR; S15289; S15289.
TIGR; HI0350; -.
                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rd."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular analysis of a complex locus from Haemophilus influ involved in phase-variable lipopolysaccharide biosynthesis."; Mol. Microbiol. 5:1013-1022(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=RM 7004 / Serotype B;
MEDLINE-92065797; PubMed=1956282;
Maskell D.J., Szabo M.J., Butler P.D.,
                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Rd
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                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random
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U32719; AAC22011.1;
 Similarity 7; Conserv
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TIGR00901;
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70.0%;
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2A0125; 1.
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DEGP_RICCN
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE008583; AAL02704.1; ALT_INIT.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; PDZ; 2.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR RC0166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
-i- SIMILARITY: BELLONGS TO PEPTIDASE FAMILY S2C.
-i- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
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Q92JA1;
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20 TGFNSGLPLF 29
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mes 6; Conserv
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GNSGGPMF 247
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508 AA; 55599 MW;
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75.0%;
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    Mismatches

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CHARGE RELAY SYSTEM (POTENTIAL).
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D2F53A690ECD0AD7 CRC64;
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PROBABLE SERINE PROTEASE DO-LIKE.

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Pred. No.
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59;
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool_VUS10008355/runat_17122002_112337_14593/app_query.fasta_1.398
-Q-/cgn2_1/USPTO_spool_VUS10008355/runat_17122002_112337_14593/app_query.fasta_1.398
-DB-GenEmbl -QFWT-fastap -SUFFIX-p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MILLEN=0 -MAXLEN=200000000
-USER-US10008355_eCGN_1_1_1616_erunat_17122002_112337_14593 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Listing first 45 summaries
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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E03836
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JP 1992211370-A/2.
Staphylococcus aureus
Staphylococcus aureus
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1 (bases 1 to 1289)

1 (bases 1 to 1289)

1 voshikawa, K., Tsuzuki, H., Fujiwara, T., Nakamura, E., Iwamoto, H.,

Matsumoto, K., Shin, M., Yoshida, N. and Teraoka, H.

Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from Staphylococcus aureus ATCC 12600

Biochim. Biophys. Acta 1121 (1-2), 221-228 (1992)
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DNA encoding V8 protease
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SHIONOGI & Co.,Ltd
Fukushima-ku, Osaka 553
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DKQQTPKIQKGCNLKPLEQCREANVILPNNDRHQITDTTNGHTA,PVTYIQVEAPTGTF
IASGVVVGKDTLLTNKHVVDATHGDPHALKAFPSAINQDNYPNGGFTAEQITKYSEGE
DLAIVKFSPNEDNKHIGEVVKPATMSNNAETQVVQNITYTGYPGDKPVATMWESKGKI
TYLKGEAMQYDLSTTGGNSGSPVFNEKNEVIGIHWGGVPNQFNGAVFINENVRNFLKQ
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/product="glutamic acid specific protease prepropeptide"
/protein_id="pax00630.1"
/db_xref="GI:216971"
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/db_xref="taxon:1280"
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OS Staphylococcus
PN JF 1992211370-
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Staphylococcus aureus.
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 1586)
Nakamura,E., Tamaki,M., Teraoka,H., Matsumoto,K.,
Fijiwara,K., Tsuzuki,H., Yoshida,N. and Kakudou,
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anti-sense: No;
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JP 1992211370-A/2
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Feature is identified by similarity;
Key Location/Qualifiers
   19-FEB-1991 JP 1991024633
20-FEB-1990 JP 90P 4039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAKUDOU SHINJI
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20-FEB-1990 JP 90P 403
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/db_xref="taxon:1280"
282 c 221 q 476 +
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/db_xref="GI:46687"

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Best Local Similarity:
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                                                                                                                                                         Submitted (16-SEP-1987) Gray G., Genencor, South San Francisco, CA 94080, USA 2 (bases 1 to 1634) Carmona,C. and Gray,G.L. Nucleotide sequence of the serine protease aureus, strain V8
                                                                                                                                                                                                                                                                                                                     SASP
Staphylococcus aureus
Y00356
                                                                                                                                                                                                                                                             Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                   serine protease.
Staphylococcus aureus
                                                                                                                                    Nucleic Acids Res. 15 (16),
87316953
                                                                                                                                                                                                                                        Gray
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C12N9/52,C12N15/57,(C12N15/57,C12R1:445);
strandedness: Double;
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hypothetical: No;
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*source: clone=pAM82SIGV8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Staphylococcus aureus"
/db_xref="taxon:1280"
302 c 219 g 476 t
/protein_id="CAA68434.1"
                              /note="preproenzyme (AA
                                             354. .1364
                                                     /db_xref="taxon:1280"
/clone="pv8CO"
                                                                             /organism="Staphylococcus/strain="V8"
                                                                                                              Location/Qualifiers
          transl_table=11/
                     /codon_start=1
                                                                                                   1. .163
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.555
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                                                                                                                                                                                                                Kimball Way,
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AF309515
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                                                                                                                                                                                                                                                                                                               Submitted (28-SEP-2000) Laboratory Medicine and Pathobiology. University of Toronto, Sunnybrook and WCHSC, 2075 Bayview Ave Toronto, ON M4N 3M5, Canada
                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 3240)
Rice, K.C. and McGavin, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      serine protease
Infect. Immun. 69 (1), 159-169 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice,K., Peralta,R., Bast,D., de Azavedo,J. and McGavin,M.J. Description of staphylococcus serine protease (ssp) operon in Staphylococcus aureus and nonpolar inactivation of sspA-encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus serine protease operon, complete sequence. {\tt AF309515}
                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/translation="MKGKFLKVSSLFVATLTTATLVSSPAANALSSKAMDNHPQQTQS
SKQQPPKIQKGQNLKPLEQREHANVILPNNDRHQITDTINGHYAPVTYIQVEAPTGTF
IASGVVVGKDTLLTNKHYVDATHGDPHALKAFPSAINQDNYPNGGFTAEQITKYSGEG
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1218. 1325
/note="twelvefold repeated tripeptide (Pro-Asp-Asn)"
1 296 c 231 g 490 t
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354. .557
                                                                                         endopeptidase"
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354. .1364
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NIEDIHFANDDQPNNPDNPNNPDNPNNPDNPNNPDEPNNPDNPNNPDNPDNSDNNNSDNPD
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/transl_table=11
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354. .1364
                                                                                                                                                                                                                                      /organism="Staphylococcus
/db_xref="taxon:1280"
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                                                                        /codon_start=1
                                                                                                              /note="serine
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Best Local Similarity:
                                  KEYWORDS
                                                                                                                      DEFINITION
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                                                                                                                                                                                                                                                   1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                          ACTGGTGGTAATTCAGGTTCACCTGTA 1076
AJ293885.2 GI:22218025
Cysteine proteinase; glutamyl endopeptidase; msrwl
proD gene; proM gene; spwl gene.
                                                                                                                    Staphylococcus warneri
                                                                                           and msrwl gene.
                                                                                                                                           SWA293885
                                                                           AJ293885
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IVYERLV"
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2103. .2624
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gene, spwl gene
                           gene;
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamakawa,A., Taketo,A. and Kodaira,K.I.
Genetic and biochemical characterization of glutamyl endopeptidase of Staphylococcus warneri M
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991. .2148
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Query Match:
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2 (bases 1 to 10689)
Simpson,A.J.G., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M.,
Alves,L.M.C., Araya,J.E., Baia,G.S., Baptista,C.S.,
Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.S.
Bueno,M.R.P., Camargo,A.A., Camargo,L.E.A., Carraro,D.M.,
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Xylella fastidiosa 9a5c
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                                                                                                                                                                              Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                and Marino, C.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE004008
                                                                                                                                   10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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IRYEKF"
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NPNDPHLGHAMAVVGNAKINNEDKLIFWNPWDTDLSIQDADSNLLHLSFNRDYTWDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="cysteine proteinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4698. .5024
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154 of 229 of the
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the Organization
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Madeira,H.M.F., Marino,C.L., Marques,M.V., Martins,E.A.L.,
Martins,E.M.F., Matsukuma,A.Y., Menck,C.F.M., Miracca,E.C.,
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Souza,A.A., de Souza,A.P., Terenzi,M.F., Truffi,D., Tsai,S.M.,
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similarity; putative; ORF located using Glimmer/RBSfinder"
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Lopes, S.A.,
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SVILDTDLGQLVRSDPSTVNAVLTDSQTGAVLLTPEIVSALNKLRRSLEDELKASHAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSVSLSSSVSSAPILGSSSVPSSH"
complement(2918. .3202)
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YYSPAHLSEAASSVAGASGQASLRAAPASLSSSRSLVSGMRTYAVLETESAPTLSGCV
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Best Local Similarity:
Query Match:
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                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                          gene
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1 ThrGlyGlyAsnSerGlySerProVal 9
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                                                                                                                                    Technology and Evaluation, Biotechnology Center; Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nitTel:81-3-3481-8423, Fax:81-3-3481-8424)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Aoki,K., Oguchi,A., Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and Kikuchi,H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus subsp. aureus MW2 (strain:MW2) DNA. Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                 Submitted (06-MAR-2002) Akio Oguchi, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     community-acquired MRSA
Lancet 359 (9320), 1819-1827 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baba, T., Takeuchi, F., Kuroda, M., Yuzawa, H., Aoki, K., Oguch
Nagal, Y., Iwama, N., Asano, K., Naimi, T., Kuroda, H., Cui, L.,
Yamanoto, K. and Hiramatsu, K.
Genome and virulence determinants of high virulence
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AP004825 BA000033
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                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 290150)
/organism="Staphylococcus
/strain="MW2"
/db_xref="taxon:196620"
285. .1493
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similarity; putative; ORF located using Glimmer/RBSfinder"
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//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAQQLMSLYCTQYDVEARTCSQQAWMVPPSLLPPISYEDVRILL
PHIVMCFLVAWGFHFLFTVVRD"
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Indels:
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                                                                                        aureus
                                                                                  subsp. aureus MW2"
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IEDTYLLMDSFISKYQDLSDVLMACGIQSERATYEFDHYKSKKKAPFKTNLNLISESL
IELDFHEGISIGQSINLARDFSNMPPNVLTPQTFAEDIVNHFKNTKVKVDVKDYDTL
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                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MW0826"
4845. .5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YETRKISDSDNVTELKPYILIVTIVAILATFLVQTFTDSMIFGALAGVLVFFISRAYN
WYELDAKFVEGIKIMAYIGVVILTANGFAGVMNATGDIDELVKTLTSITGDNKLFSII
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VLLPYGEGQIFQQIIQSGFAKANHPIEFNMIWKAMLIPSMGYIVGLLIGLYVYYKKPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MW0825"
3510. .4826
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VEVMNTDAEGRLVLADAVFYANQYQPSVIMDFATLTGAAIVALGDDKAAAFESNSKVI
LNDIIQISSEVDEMVFELPITATERASIKHSDIADLVNHTNGQGKALFAASFVTHFSG
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yeatmlheasagtlayedvlkpvesvlkkdkvnfvqaevtkldbakkvetnogaiydf
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1624. .3099
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                                                                              complement(5275. .6429)
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                                                        /gene="MW0827"
                                                                                                                                                                                                                                                                                                                                                                     /note="ORFID:MW0826"
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                                                                                                      gene
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                                                                                                      complement(9275.
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VFATKAGVEPMEVWLPSAYYAPPIPIIAFEGALLTKVGVYAINRTLSLFFSDAVSFSH
VYILFIALLTIIFGCVGAVAXANIKKIILYNVMIAVGVILVGVAMMTESGMIGAIYTT
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QNVNHIFFKEHDQVVYDKTDHIVGSGITAAHLALKLLNHDNUKKIHLWLNKDIEIHDF
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STLGAMSLLFGTFLYFIATQGFVNMQLIVAIIFVLITGPLSSHMIMKAAYNIKTPYTK
KTKVDEISEDLKDTKL"
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FYGKFFIVQSTFERGFYLSGVIVLLSSLVVLYSVIRIFLQGFFGQPKGYDLNNKVDVK
YLTTIAIVAVVITVLYGLSADYLYPMVKAGAETFYNPSTYVKAVLGGK"
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/gene="mnhE"
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/protein_id="BAB94694.1"
/db_xref="GI:21203996"
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/gene="mnhf"
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TPITQISDGLINTENNSVPYQQIMVATGFEQDEMSQPLIKQLIQNYDAPINECNYPVI
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/db_xref="GI:21203997"
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                                            Submitted (30-JAN-2001) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Mishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13700734.
                                                                                                                                                                                                                                       2 (bases 1 to 298050)
Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K.
and Kikuchi,H.
                                                                                                                                                                                                                                                                                                                                                                                                    Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J., Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K. Whole genome sequencing of meticillin-resistant Staphylococcus
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani'Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain:N315) DNA.
Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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AP003132.2 GI:14349174
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TMGGLKHGTVPLIYEANVKSYVDPIPQALILTAIVIAFATTAFFLVLAFRTYKELGTDN
VESMKGVPEDD"
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/gene="mnhB"
/organism="Staphylococcus aureus subsp. aureus N315"
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.FASSLVIITIAFDIETMRKIFPLDFKILIGIGLVFCIATPIASWFLGKNFFTHVTFD
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                                                                                                                                                                                                                                                                                                                                                                                                    /gene="dltC"
3134. .3370
/gene="dltC"
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1902. .3116
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LVQFTEMMLELMKSGNKQQMLKQAPFSEDLSVMAIVPCLASGGTLNJVDKNMINKPKL
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FPSATIYNTYGPTEATVAVTSIQITQEILDQYPTLPVGVETLGARLSTTDDGELVIEG
QSVSLGYLKNDQXTAEVFNEDDGILTTYHTGDKAKFENGQWFIQGRIDFQIKLNGYRME
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/translation="METREQVLNLLAEVAENDIVKENPDVEIFEEGIIDSFQTVGLLL
EIQNKLDIEVSIMDFDRDEWATPNKIVEALEELR"
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/db_xref="G1:13700737"
/db_xref="G1:13700737"
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PLALVKVLQSTWLGGHQIHFHESKLIEFVGFLGISYVTFKSVQLIMEIRDGSIKEIKV
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280. .
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                                                                                                                                       /gene="dltD"
3367. .4542
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FDKPFKAKNIKDFWNRWHMTLSFWFRDCIYMRSLFYMSRKKLLKSQFAMSNVAFLINF
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448. .1905
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                   /note="ORFID:SA0795"
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JOURNAL
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                                                                                                                                                                                           Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan (E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454, Fax:81-298-53-3454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus subsp. aureus sequence, section 4/9.
AP003361 BA000017
AP003361.2 GI:14246761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M., Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A., Mizutani-Ui, Y., Takahashi, N.K., Sawano, T., Inoue, R., Kaito, C., Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Kanahisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C., Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H., and Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain:Mu50) DNA.
Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphy
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                                                                                                                                                                           29,
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35. .1021
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7973. .9181
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VLSWGGIARLYRGKVLQEKENEFYFLAAKSIGTPTYKIILKHLLPNILSVVIVQATLLF
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2971. .3852
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2971. .3852
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35. .1021
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1997. .2959
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1024. .2004
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1024. . 2004
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5943. .6662
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6783. .7769
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MDEINEEEDFVVEGPLWIQVHAFEKGVEVTISKSK NEDMMNWSDDATDQFDEGVVGEL
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5177. .5572
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Chicago, 840 S. W
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AF008576
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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840 S. Wood St. (M/C 787),
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                                                                                                                                                                                                                                                                  Direct Submission Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (21-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                           Submitted (20-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri On Mar 11, 2002 this sequence version replaced gi:186935
                                                                                                                                                                                                                                                                                                                                                           MO 63108, USA
5 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (24-CAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 162609) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
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Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                           Direct Submission
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AC108022.3 GI:19
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Center project name: H_NH0009D08
Drafting Center: WIBR
                                                      Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
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BAC clone RP11-9D8
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                                                                                                                                                                                                                                                                                   Louis,
                                                                                                                                                                      USA
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence may not represent the entire insert of this

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The clone sequenced to the left is RP11-36B15; the clone sequenced to the right is RP11-77C12, 2000 bp overlap. Actual end of this clone is at base position 12410 of RP11-177C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y. Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
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   Location/Qualifiers
                  /rpt_
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4170.
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(NID:g14427375)"
2689. .2836
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4513. .4550
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329. .510
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/db_xref="taxon:9606"
/chromosome="4"
'note="match to EST BE172154 (NID:g8634880)"
                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match to EST
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                                  _family="MIR"
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                                                               Best Local Similarity:
Query Match:
              US-10-008-355-26 (1-9) x AC108022 (1-162609)
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17656. .17
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13268. 13339
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19184. .19456
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17867. .17961
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15257. .15567
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14279. .14373
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11533. .11838
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10967. .11016
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10662
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10337. .10648
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13062. .13216
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3292. .8347
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Matches:
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FEATURES

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                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 163223 bases at least Q40
Consensus quality: 164704 bases at least Q30
Consensus quality: 165029 bases at least Q30
Consensus quality: 165029 bases at least Q20
Estimated insert size: 179000; agarose-fp estimation
Quality coverage: 8.17 in Q20 bases; agarose-fp estimation
Quality coverage: 8.78 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: CITB-H1_2210F7
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DOE Joint Genome Institute.
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AC108085.1 GI:18369931
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                                                                                     53321
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                                                                                 /clone="CTD-2210F7"
/clone_lib="CalTech human BAC 32702 c 32339 g 48053 t
                                                                                                                                                 /chromosome="5"
                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                              1111: contig of 1111 bp in length
1231: gap of unknown length
2531: contig of 1320 bp in length
2631: gap of unknown length
4084: contig of 1453 bp in length
4184: gap of unknown length
50656: contig of 46472 bp in length
50756: gap of unknown length
101216: contig of 50460 bp in length
101316: gap of unknown length
16978: contig of 65662 bp in length
Length:
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AC036185
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.yenome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 21, 2000 this sequence version replaced gi:7523854.
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Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reassembly program: Phrap; version 0.960731 Consensus quality: 163254 bases at least 040 Consensus quality: 166954 bases at least 030 Consensus quality: 168680 bases at least Q20 Insert size: 170000; agarose-fp
                                                                                                                                                                                                                                                                                 Center project Information Center project name: L9247 Center clone name: 679_B_6
                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
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28994 39086: contig of 10093 bp in length
39087 39186 gap of 10093 bp in length
50078 50177: contig of 10891 bp in length
50178 61526: contig of 11349 bp in length
61527 61626: gap of 100 bp
61627 75529: contig of 13903 bp in length
75530 75629: gap of 100 bp
75630 91544: contig of 13915 bp in length
91545 91644: gap of 100 bp
91645 108750: contig of 17106 bp in length
108751 108850: gap of 100 bp
118877: contig of 17106 bp in length
136878 136977: gap of 100 bp
136878 136977: gap of 28027 bp in length
136878 17177; gap of 34302 bp in length
136978 171779 gap of 100 bp
136978 17179: contig of 34302 bp in length
1000 pp
1000 pp
11000 pp
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Quality coverage: 7.1 in Q20 bases; agarose-fp
Quality coverage: 7.1 in Q20 bases; sum-of-contigs
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4209 7507: contia of 7508 7607
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1386 1485: gap of 100 bp
1486 2835: contig of 1350 bp in length
2836 2935: gap of 100 bp
2936 4108: contig of 1173 bp in length
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7508 7607: gap of 100 bp
7608 13869: contig of 6262 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="4
                                       /note="assembly_fragment"
61627. .75529
                                                                                                       /note="assembly_fragment" 50178. .61526
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39187. .50077
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13970. .20810
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                              'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="RP11-679B6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110: gap of 100 bp 28893: contig of 7983 bp in length 93: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp 20810: contig of 6841 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .7507
                                                                                                                                                                                                                                                     .39086
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .13869
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100 bp
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KEYWORDS
SOURCE
ORGANISM
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VERSION
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AC068590
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Best Local Similarity:
Query Match:
                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 126420
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                                                                                                                                                                                                                                          TITLE
                                                                                                     AUTHORS
                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Callymore, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gand, Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarrhe, M., McCarrhe, M., McCarrhe, M., McCarrhe, R., Landers, R., McCarrhe, K., McCarrhe, McCarrhe,
                                                                                                                                                                                                                                                                McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Voung,G., Zalnoun,J., Zimmer,A. and Zody,M.
                         Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                      Submitted (04-MAY-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 8, clone RP11-131K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 174253)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, 30 unordered
AC068590
AC068590.2 GI:8389591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48027
                                                                                                                                  (bases 1 to 174253)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
91645. .108750
/note="assembly_fragment"
108851. .136877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector_side:right"
136978. .171279
/note="assembly_fragment"
1 36049 c 36303 g 49499
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100.00%
91.67%
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44.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174253 bp DNA linea chromosome 8 clone RP11-131K16 map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .91544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
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Conservative:
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Colangelo, M., Collins, S.,
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6 map 8,
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WORKING DRAFT
                                                                                                                                                                                                          for Genome
                                                                                                     Allen, N.
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., McMara, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., McCarthy, P., Rothman, D., Pollara, V., McCarthy, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, P., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, P., Rogov, P., Rothman, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 9, 2000 this sequence version replaced gi:7705204. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                      5628 5727; contig of 203 bp in 16
5628 5727; gap of 100 bp
5728 7753; contig of 2026 bp in 16
5728 7753; contig of 2026 bp in 16
7754 7853; gap of 100 bp
7854 7853; gap of 100 bp
9492; contig of 1639 bp in 16n
9493 9592; gap of 100 bp
9593 11429; contig of 1837 bp in 16ng
11430 11529; gap of 100 bp
11530 13178; contig of 1649 bp in 1-
3179 13278; gap of 100 bp
3179 13278; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 170000; agarose-fp Insert size: 171353; sum-of-contigs Quality coverage: 3.5 in Q20 bases; Quality coverage: 3.5 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.960731
Consensus quality: 156518 bases at least Q40
Consensus quality: 165902 bases at least Q30
Consensus quality: 169236 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; M77815; 100
Chemistry: Dye-terminator B1g Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L9496
Center clone name: 131_K_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preserved.
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3435 5627: contia of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1232: contig of 1232 bp in length
1233 1332: gap of 100 bp
1333 3334: contig of 2002 bp in length
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   20019: gap of
22351: con
                                                                                                                                             16053: gap of 
18335: con
                                                                                                                18435:
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                                                                 18335: contig of : 435: gap of : 19919: contig of :
                                                                                                                                                                                                           78: gap of 100 bp
15953: contig of 2675 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project Information
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                                                                                                                                                                              100 bp
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137393 137492:
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72008 79155: contig of 7148 bp in length
79156 79255: gap of 100 bp
79256 88577: contig of 9322 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65256 65355:
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                                                             /note="assembly_fragment"
22452. .25473
                                                                                                                                                                   vector_side:right"
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1333. .3334
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/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                        note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5875: gap of 11
52390: contig of 1
2490: gap of 1
57638: contig of 1
7738: gap of 1
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174253: conti
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71907: contig of
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f 9322 bp in length
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of 5515 b
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Pred. No.: 1.95e+04
Score: 44.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 91.67%
DB: 2
Search completed: December 20, 2002, 15:04:09 Job time : 1506.26 secs
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                                                                                             US-10-008-355-26 (1-9) x AC068590 (1-174253)
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32675. 36983
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41658. 46775
/note="assembly_fragment"
46876. .52390
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Result
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Maximum DB seq
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Perfect score:
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     SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
11: sp_virus:'
13: sp_verteb)
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   5 Q9PC94
Q47809
5 Q98MQ9
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Q04186
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38.381 Million cell updates/sec
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O8ve75 mus musculu
O9d219 mus musculu
O9d219 mus musculu
O9dkc9 rhizobium 1
O8ym87 anabaena sp
O8xhm4 clostridium
O9zdx8 rickettsia
O62313 mus musculu
O62314 mus musculu
Q92j35 rickettsia
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Q47809 enterococcu
Q98mg8 rhizobium l
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Q9ajx0 staphylococ
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Q99v45 staphylococ
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Q53782	Q9KH49	Q99T60	Q9FD08	Q9KH51	Q9LA54	Q9LA58	Q8RY22	Q9SRP2	Q9FYL4	Q8RE47	Q9E960	Q66149	Q89504	Q9KLD4	Q9RTZ8	Q9FMX1	Q8TZS8	Q8QR15	098в89	P96151	074325	Q9P7S1	Q9LK70	Q8VA04	168460	Q8YFB1	Q9A9N9	Q92LB9
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Q53782 staphylococ		Q99t60 staphylococ	Q9fd08 staphylococ	Q9kh51 staphylococ	Q91a54 escherichia	Q91a58 escherichia	Q8ry22 arabidopsis	Q9srp2 arabidopsis	ırabidopsi	Q8re47 fusobacteri	Q9e960 cocksfoot m	Q66149 cocksfoot m				щ		G	9		074325 schizosacch	ß	arabio	Q8va04 apple stem	Ω		Q9a9n9 caulobacter	Q921b9 rhizobium m

ALIGNMENTS

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Q9FBG1
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AC Q9FBG1;
AC Q9FBG1;
DT 01-MAR-2001 (TrEMBLrel. 16, C:
DT 01-MAR-2002 (TrEMBLrel. 20, L
DT 01-MAR-2002 (TrEMBLRel. 20, L
                                                 RESULT 1
 Query Match
Best Local Similarity
Matches 10; Conserv
                                               Pfam; PF00089; trypsin; I.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPC: 1.
PROSITE; PS50240; TRYPSIN_DOM; 1
PROSITE; PS50673; V8_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 316 AA; 34296 MW; 4.
                                                                                                                                                          Staphylococcus warneri M.";
Submitted (SEP-2000) to the
EMBL; AJ293885; CAC06168.1;
MEROPS; S01.269; -.
                                                                                                                                                                                                                                                                                                                       Staphylococcus warneri. Bacteria; Firmicutes; E Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                            PROM.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1292;
[1]
                                                                                                                                                                                                                                                                                                                                                                      Glutamyl endopeptidase.
                                                                                                                                  InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000126; Ser_proteas_V8.
                                                                                                                                                                                                                       Kodaira K.I.;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Submitted (AUG-2000) to the
                                                                                                                                                                                                                                                                       Kakikawa M.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                           "Characterization of the
  Conservative
            100.0%;
                                                                                                                                                                                                                                                                                                                                  Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                   gene encoding glutamyl endopeptidase
 0;
                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
            Score 54; DB 2; Length 316; Pred. No. 0.15;
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                                               4E997A5A111DDB40 CRC64;
 Mismatches
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Best Local
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InterPro; IPR00125; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
PRINTS; PR0083; V8PROTEASE.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
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01-JUN-2001 (TrEMBLrel. 17, Crei
01-JUN-2001 (TrEMBLrel. 21, Las:
01-JUN-2002 (TrEMBLrel. 21, Las:
Serine protease, V8 protease, g
SSPA OR SAV1048 OR SA0901.
                                                                                                                                                                                            Q04186 PRELIMINARY; PRT; 357 AA. Q04186; Q14186; Q1-NOV-1996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update) Q1-NOV-1996 (TrEMBLrel. 20, Last annotation update Glutamic acid specific protease prepropeptide (EC)
                                                                                                                                                                               Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-21311952; PubMed=11418116;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K. I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakani H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSPA OR SAV1048 OR SAUYU1.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                    Staphylococcus.
                                                                                                                                                         Bacteria; Firmicutes;
     Matsumoto
                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99V45
                                                                                                          NCBI_TaxID=1280;
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                             Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.269;
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N.A.
Tsuzuki H., Fujiwara
Shin M., Yoshida N.,
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36977 MW; 5AEF42DCE01C4B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                       Bacillus/Clostridium
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Pred. No. 0.17;
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                     Τ.
  T., Nakamura
Teraoka H.;
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                                                                                                                                                       group;
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                                                                                                                                                         Bacillales;
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                             Iwamoto H.
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RESULT 5

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Q9PC94 PRELIMINARY; Q9PC94; 01-OCT-2000 (TrEMBLrel. 15,

Created)

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                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                SIGNAL
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InterPro; IPR000126; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL; AJ305145; CAC27157.1; HSSP; P09331; 1EXF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00673; V8_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=6746;
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InterPro; IPR000126; Ser_proteas_V8.
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EMBL; D00730; BAA00630.1;
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167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis extracellular serine proteinase.";
submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                            2 GGNSGSPVF 10
GGNSGSPVF 175
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                                                                                                                                    similarity
9; Conserv
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357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease;
                                                                                                                                                                                                                                                                            217 AA;
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                        217
23667
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                                                                                                                                                                 90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.
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                                                                                                                                                                                                                                                                            MW;
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                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
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                                                                                                                                                                    Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                         EXTRACELLULAR SERINE PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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                                                                                                                                                                                                                                                                        FB9B886D453B8BB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58AA9A4E371E2577 CRC64;
                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                    DB 2;
0.79;
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(Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
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                                                                                                                                                                                                 Length 217;
                                                                                                                                                                                                                                                                            CRC64
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                                                                                                                                    Indels
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RA Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Array J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.E.R.,
RA Coutinho L.L., Cristofani M., Dias-Meto E., Docena C., El-Dorry H.,
RA Coutinho L.L., Cristofani M., Dias-Meto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.Y.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto J.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Quaggio R.B., Roberto P.G., Rodrígues V., de Rosa A.J.M.,
A de Sliva M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Silva M.C., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Good M.A., Zatz M., Meidanis J., Setubal J.C.,
"The genome sequence of the plant pathogen Xylella fastidiosa.";
RDMAINGAL ALEGA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
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                  STRAIN=OG1-10;
Su Y.A., Clewel
"A gene (sprE)
                                                                                                                                                                                              01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                               Q47809
Q47809;
                                                                                                                                 Enterococcus faecalis
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20365717; PubMed=10910347;
Simpson A.J.G., Reinach F.C., Arruda P.,
                                                                SEQUENCE FROM N.A.
                                                                                                                  Enterococcaceae;
                                                                                                                                                                             Staphylococcal serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete SEQUENCE 716 AA; 79375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004008; AAF84693.1; -. MEROPS; S46:001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein XF1887.
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                             647
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 9; Conserv
             Y.A., Clewell D.B.;
gene (sprE) downstream of
                                                                                                                                                                                                                                                                                                                                                                           1 TGGNSGSPV
                                                                                                                                                                                                                                                                                                                                           TGGNSGSPV 655
   serine
                                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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ownstream of gelE of Enterococcus faecalis OG1-10 proteinase determinant of Staphylococcus aureus
                                                                                                                Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xf1887
                                                                                                                              (Streptococcus faecalis). Bacillus/Clostridium grou
                                                                                                                                                                           1. 01, Created)
1. 01, Last sequence up
1. 21, Last annotation
proteinase homologue.

    Last sequence update)
    Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48;
Pred. No
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EAF086E2315BBDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       No.
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4;
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                                                                                                                                                                                            on update)
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                                                                                                                              group;
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 716;
                                                                                                                                Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT
Q8VE75
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                             Q8VE75;
Q8VE75;
01-MAR-2002
01-MAR-2002
                                                        01-MAR-2002 (TTEMBLrel 20, Created)
01-MAR-2002 (TTEMBLrel 20, Last sequence update)
01-MAR-2002 (TTEMBLrel 20, Last annotation update)
01-MAR-2002 (TTEMBLrel 20, Last annotation update)
Similar to RIKEN cDNA 4632417K18 gene (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                              EMBL; AP002995; BAB48055.1; -. Hypothetical protein; Complete SEQUENCE 289 AA; 31310 MW;
                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasan Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno P. Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical MSL8587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q98MQ8;
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001254; Ser_protease_Try
InterPro; IPR000126; Ser_proteas_V8.
PRINTS; PR00839; V8PROTEASE.
                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80W860
SEQUENCE FROM N.A
                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                   DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21082930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phyllobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain V8.";
                                                                                                                                                                                                                                                                                                                                                 Mesorhizobium loti."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224
                                                                                                                                                                                                194 GGSSGSPVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGGNSGSPVF
||| |||::
|224 TGGQSGSPIY
                                                                                                                                                                                                                        N
                                                                                                                                                                                                                      GGNSGSPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conserv
                                                                                                                                                                                                                                               Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                   7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
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                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11214968;
                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31063 MW;
                                    Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                            81.5%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ms18587.
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                                                                                                                                                                                                                                                         Score 44; I
Pred. No. 7.
                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae: Mus
                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D4F0312BEE778415 CRC64;
                                                                                                                                                                                                                                                                                            proteome.
8947CDDFC6BC0253 CRC64;
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7.9;
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                                                                                                                                                                                                                                                                                                                                                            symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                   Sugimoto M.,
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Q9D2L9
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Best Local Similarity
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RC STRAIN=CS7BL/60; TISSUE=SKIN;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Arakawa T., Hara A., Fukunishi Y., Rasukawa T., Saito R.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Kadota K., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gansterland T., Washio T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Washio T.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Basaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashtaki Y., Storch
                                                                                                                                                                                      Matches
                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrembLrel. 1
01-JUN-2001 (TrembLrel. 1
01-JUN-2001 (TrembLrel. 1
4632417K18R1K protein.
4632417K18R1K.
              Q98KC9;
Q98KC9;
01-OCT-2001
01-OCT-2001
01-MAR-2002
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Submitted (DEC-2)
EMBL; BC019638;
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Metazoa; Chordata,
Metazoa; Rodentia;
                                                                                                                                                                                                                                                            EMBL;
   Hypothetical
                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK019499; BAB31763.1; -
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                                                                                                                                                                                                                                                                                        *Functional annotation
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ENCE 613 AA; 69948 MW; 1
                                                                                                                                                                                   Similarity
8; Conserv
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(DEC-2001)
  (TrembLrel. 18, C
(TrembLrel. 18, L
(TrembLrel. 20, L
L) (TrembLrel. 30, L
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88.9%;
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88.9%;
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17,
17,
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                                         Created)
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Q8XHM4
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Q8YM87
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Q8XHM4;
Q8XHM4;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Q8YM87;
01-MAR-2002
01-MAR-2002
01-MAR-2002
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Hypothetical
SEQUENCE 10
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SEQUENCE 1
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DNA Res. 7:331-338(2000)
                                                                                                                     109
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8; Conserv
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                          (TrEMBLrel.
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                                                     PRELIMINARY;
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Nakazaki N., Shimpo S., Sugimoto M., Takazawa Makazaki N., Tabata S.;
"Complete genomic sequence of the filamentous regranobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003598; BAB76748.1; -
                                                                                                                                                                       Watanabe A., Irigucuz ....
Watanabe A., Kohara M., Matsumoto
Kishida Y., Kohara M., Matsumoto
Nakazaki N., Shimpo S., Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21082930; PubMed=11214968; Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasai Kaneko T., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLL1534.
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                          MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P.,
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AP002997; BAB48885.1; -.
Chetical protein; Complete;
Chetical protein; 100023 MW;
                                                                     169 AA; 17427 MW;
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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Iriguchi M., Ishikawa
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                  7.8%;
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Pred. No.
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L; Mismatches
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                                                                     proteome.
0A610CC04EE4C48A CRC64;
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; AC3F2877D0B94C53 CRC64;
 Mismatches
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M., Matsuno A., I
M., Takazawa M.,
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1;
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i K., Kimura (
                                Length 169;
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01-MAY-1999
01-MAY-1999
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondria.";
Nature 396:133-140(1998)
                                                                                                                                                                                                                                                                IMBL; AU43/4/V, T. IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the sequence of Rickettsia prowazekii and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-MADRID E;
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
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PubMed=11792842;
Shimia
                                                                                                                                                                                                  PROSITE; PS50106; PDZ; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                              Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: TO SERINE PROTEASES, EMBL; AJ235270; CAA14652.1; -.
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Pfam; PF02875; Mur_ligase_C; 1.
TIGRFAMS; TIGR01087; murD; 1.
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Clostridiales; Clostri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99039499; PubMed=9823893;
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MURD OR CPE2459.
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                                                 8; Conserv
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315 AA; 35033 MW;
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gasawara N., Hattori M., Kuhara S., Hayash
enome sequence of Clostridium perfringens,
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Clostridiaceae; Clostridium.
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88.9%;
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70.0%;
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eae; Rickettsia.
                                                                                                                                         Complete proteome. W; 2D91A0D54FFBE9A1 CRC64;
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Last annotation updat
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                                                   0;
                                                                        Score 40;
Pred. No.
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Pred. No.
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                                                                                               Length 315;
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RESULT 14
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Best Local S
Matches 7
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Q62313;
Q62313;
Q1-007-1996 (TrEMBLrel. 01, Created)
Q1-007-1996 (TrEMBLrel. 01, Last sequence update)
Q1-007-1996 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trans-901gi network integral membrane protein TGN38A
golgi network protein 1) (TGN38 homolog).
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                                                                                                                                                                                                                                          CARBOHYD
SEQUENCE
Q62314 PRELIMINARY;
Q62314;
Q1-NOV-1996 (TrEMBLrel. 01,
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REPEAT
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REPEAT
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REPEAT
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GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NE
SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).
-i- TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2001) to the E -!- FUNCTION: MAY BE INVOLVED FROM TRANS-GOLGI NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE=BRAIN;
MEDLINE=95301533; PubMed=7540170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Mus musculus (Mouse).
'`~rvota; Metazoa; Chordata; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Transmembrane; Glycoprotein; SIGNAL 1 17 POTENTIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kasai K., Takahashi S., Murakami K., Nakayama K.
Strain-specific presence of two TGN38 isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
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7; Conserv
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87.58;
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                                                                                                                                                                                                                                            MW.
                                                                                                                                                                            0;
                                                                                                                                                                                            Score 40;
Pred. No.
                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
; 95C340C2F4A21EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY).
6 X 8 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                                    PRT;
                                                                                                                                                                              Mismatches
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                                    363
                                    AA.
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; Murinae; Mus
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Search completed: December 20, 2002, 12:10:18 Job time: 63.6842 secs
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Best Local Similarity
Matches 7; Conserv
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CARBOHYD
SEQUENCE
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J. Biol. Chem. 270:14471-14476(1995).

J. Biol. Chem. 270:14471-14476(1995).

FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TRAFFIC TO AND FROM TRANS-GOLGI NETWORK.

FOR TRANS-GOLGI NETWORK.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PRIMARILY IN TRANS-GOLGI NETWORK CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND THE CELL SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).

-!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                         Signal; SIGNAL
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SITE
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-BRAIN;
MEDILINE-95301533, PubMed-7540170;
Kasai K., Takahashi S., Murakami K., Nakayama K.;
"Strain-specific presence of two TGN38 isoforms and absence of TGN41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trans-golgi network integral membrane protein TGN38B precursor (Trans-golgi network protein 2) (TGN38 homolog).
TGOLN2 OR TTGN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                  EMBL; D50032; BAA08758.1; -. MGD; MGI:105079; Tgoln2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                140 TGGNSGKP 147
                                                                       1 TGGNSGSP 8
                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein; Repeat; Golgi stack.

1 17 POTENTIAL.
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363
                                                                                               Conservative
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                                                                                                                                              38821 MW;
                                                                                                         74.1%;
87.5%;
                                                                                             0;
                                                                                                         Score 40; DB 11;
Pred. No. 50;
                                                                                                                                            N-LINKED (GLCNAC. . .) (P
; 2826FA9E958C5C27 CRC64;
                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY).
7 x 8 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                 TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38B.
                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                               Mismatches
                                                                                             1;
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Result
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Perfect score:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
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                        US-09-221-017B-726

US-09-221-017B-1045

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US-09-071-035-427

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US-08-225-224-31

US-08-722-258-31

PCT-US95-04468-31

US-08-722-258-28

US-08-722-258-28
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  US-08-998-416-856
              PCT-US95-04468-28
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Compugen Ltd
Sequence
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                                     726, App
1045, Ap
892, App
427, App
425, App
31, Appl
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28, Appl
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9-227-357-4	-09-182	-09-568-059-	-09-165-240-	-09-182-145-3	-08-998-416-2	9-171-209-	9-328-111-2	7-624-313-	8-549-757A-	9-342-681C-9	9-364-539-5	9-364-539-5	-09-091-814-1	09-091-814-10	28147-	-08-673-768-	-08-673-768-	8-232-016-	-08-232-016-2	S-09-194-905-	-09-025-583	-08-351-413-	9-084-889-	-08-475-975-	8-478-015-	8-064-121-	8-914-848-2	7-952-853-2	7-723-002C-	S-09-221-017B	-08-680-326-11	35-634-
equence 43, App	e S	equence 1, Appl	equence 1, Appl	equence 38,	equence 262, Ap	equence 53,	equence 290, Ap	equence 3, Appl	equence 13, App	uence 94,	equence 59, App	equence 58, App	equence 109, Ap	equence 104	Lent No., 542814	1, Appl	, Appl	22, App	equence 23,	equence 7, Appl	e 2, Appl	equence 2,	equence 1, Appl	equence 1,	e 1, Appl	equence 1, Appl	e 21, App	e 21,	equence 5, Appl	38,	118, Ap	: 1, Ap

ALIGNMENTS

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RESULT 1
US-09-221-017B-726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 726, Application US/09221017B Patent No. 6444799
GENERAL INFORMATION:
                                                                                                                                                                                                                                         OPERATING SYSTEM: Wind
SOFTWARE: FastSEQ for
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
           APPLICATION NUMBER: IFILING DATE: 09-APR-PRIOR APPLICATION DATA:
APPLICATION NUMBER: IF
                                                                       APPLICATION NUMBER: PP15-
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
                                                                                                                           FILING DATE: 31-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ross, Bruce C
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                           FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                        STREET: 755 PAGI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MOKKLEON COMPRET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                         MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                         Diskette
                                             09-APR-1998
10-DEC-1998
                                                                                                                                                                                                          23-DEC-1998
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                                                                                                                                                                                                                                                                           Windows
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             PCT/AU98/01023
                                                                PP2911
                                                                                                             PP1546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GINGIVALIS NUCLEOTIDES AND USES THEREOF
                                                                                                                                                                                                                                                          Version 2.0b
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ATTORNEY/AGENT INFORMATION:

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US-09-221-017B-1045

Sequence 1045, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650-813-560
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                 PRIOR APPLICATION DATA:
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                                                                               APPLICATION NUMBER: PP15: FILING DATE: 30-JAN-1998
                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 23-DEC-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MURKLOUN COMPRET: 755 PAGE MILL ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ropology:
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100.00%
100.00%
PCT/AU98/01023
                                                                                                    PP1546
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                   US-10-008-355-26 (1-9) x US-09-134-001C-892 (1-936)
                                                                                                                                                      Score:
                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                   SEQ ID NO 892
LENGTH: 936
TYPE: DNA
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APPLICANT: LYDD DOUGETTE-SLAMM ET AL
APPLICANT: LYDD DOUGETTE-SLAMM ET AL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2384 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
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706141
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1...2384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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2 GlyGlyAsnSerGlySerProVal 9
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43.00
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100.00%
89.58%
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48.00
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FR: 27340-20021.00
                                                                                   Gaps:
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Matches:
                                                                                                  Mismatches:
Indels:
                                                                                                                                   Matches:
Conservative:
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US-09-071-035-425
; Sequence 425, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-071-035-427
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                             ADDRESSEE: Human Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                575
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OPERATING SYSTEM:
SOFTWARE: ASCII'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
                             CITY: Rockville
STATE: Maryland
                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                 COUNTRY:
                                                                                                                                                                                                                                                                                             1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                               ACCGGCGGTCAATCTGGTTCACCAATC 601
                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
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20850
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                                                           9410 Key West Avenue
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               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                             Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (301) 309-8504
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85.42%
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Matches:
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Indels:
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Best Local Similarity:
Query Match:
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ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
CLASSIFICATION: 530
                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC -DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 888 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KREITMAN, RObert J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703 ACCGGCGGTCAATCTGGTTCACCAATC 729
                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: HP Vect
OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/071,035
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                                                                                                                                                                                                                                                                  94105-1493
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                     15280-193
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TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:

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Best Local Similarity:
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                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION UMBER: WO PCT/US95/04468

FILING DATE: 06-APR-1995

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/225,224

FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 015280-193100US

TELEPAN: (415) 576-0300

TELEPAN: (415) 576-0300

INFORMATION FOR SEQ ID NO: 31:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kreitman, Robert J.
APPLICANT: Puri, Raj K.
TITLE OF INVENTION: Circularly Permuted Ligands and
TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pastan, Ira
                               MOLECULE TYPE:
                                                                                                                   SEQUENCE CHARACTERISTICS:
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CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/722,258 FILING DATE: 08-JAN-1997
NAME/KEY:
                                               TOPOLOGY:
                                                              STRANDEDNESS:
                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                             nucleic acid
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                                                 linear
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RESULT 9
US-08-225-224-28
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; Sequence 31, Application PC/TUS9504468
; GENERAL INFORMATION:
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Query Match:
                                                                                                                                                                            US-10-008-355-26 (1-9) x PCT-US95-04468-31 (1-39)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 31:
Sequence 28, Application US/08225224 Patent No. 5635599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
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MEDIUM TYPE: Floppy disk
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FILING DATE: 07-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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Conservative:
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US-08-722-258-28
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Best Local Similarity:
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US-08-225-224-28
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                                                                                                                                                                                                                                                                                         Patent No. 6011002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               Sequence
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ATTORNBY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                     TITLE OF INVENTION: Circularly Permuted TITLE OF INVENTION: Circularly Permuted NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         APPLICANT: Pastan, Ira
APPLICANT: Kreitman, Robert J.
APPLICANT: Puri, Raj K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: KREITMAN, ROBERT J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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TYPE: n
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STATE: California
                                                                                                  CITY: San Francisco
STATE: California
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FILING DATE: 8-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                    COUNTRY:
                                                                                                                                      STREET:
                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
                                                                                                                                    E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                    USA
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PC-DOS/MS-DOS
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Matches:
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9043
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Weber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 08-JAN
                                                                                                                                                                                         FILING DATE: 0'CLASSIFICATION:
                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 42 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/225,224 FILING DATE: 08-APR-1994
                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThrGlyGlyAsnSerGlySerPro
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59
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                                                                                                                                                                                                                                                            Release #1.0, Version
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                                                                      15280-193-1PC
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US-08-998-416-856/c
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CT-US95-04468-28
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Patent No. 62
                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-30

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wendianu, APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
ADDRESSEE: No. 6239264artis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                             SEQUENCE CHARACTERISTICS:
LENGTH: 743 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLFCHITC.
             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                 FILING DATE: 24 CLASSIFICATION:
ORGANISM:
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                                                                                                                                                 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pohlmann, Rainer
Steiner, Sabine
 PAG1539UP
                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
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                               DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                 24-DEC-1997
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Matches:
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Indels:
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US-10-008-355-26 (1-9) x US-08-998-416-856 (1-743)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: 07/782,372

APPLICATION NUMBER: 07/782,372

FILING DATE: 24-OCT-1991

APPLICATION NUMBER: Japanese Patent
APPLICATION NUMBER: Application No. 5459064 2-288110

FILING DATE: October 24, 1990

ATTORNEY/AGENT INFORMATION:

NAME: BOZICEVIC, KARL

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 29900-20298.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415, 677-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08035634
Patent No. 5459064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 677-7522
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     TOPOLOGY: line
MOLECULE TYPE: gr
ORIGINAL SOURCE:
ORGANISM: Baci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: EPSON PC 286 BOOK type laptop OPERATING SYSTEM: MS-DOS 2.11 SOFTWARE: Wordstar 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHIONOGI & CO.,
TITLE OF INVENTION: A NO. !
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     576 ACCGGTGGTGGATCTGGAGGACCTATA 550
                                 NAME/KEY: mature peptide LOCATION: 605 to 1270
                                                                          NAME/KEY: signal peptide LOCATION: 323 to 604
                                                                                                                                                                                                   ORGANISM: Bacillus licheniformis STRAIN: ATCC NO. 14580
                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/035,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 545 Middlefield CITY: Menlo Park
OTHER INFORMATION:
                                                                        IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
               IDENTIFICATION METHOD:
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323 to 1270
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               by experiment
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Conservative:
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Best Local Similarity:
Query Match:
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                  Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-008-355-26 (1-9) x US-08-035-634-1 (1-1448)
                              Best Local Similarity:
                                              Percent Similarity:
                                                            Score:
                                                                           Pred. No.:
                                                                                         Alignment Scores:
                                                                                                                      US-08-680-326-118
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Patent No.
                                                                                                                                                                                                                       TELEFAX: (415) 494-079
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: //
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                               REEFRENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                   NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GlyGlyAsnSerGlySerProVal 9
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5. 5925733
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TODARO, GEORGE J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOSCH, MARNIX
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                                                                                                                                                CDS
                                                                                                                                   2..454
                                                                                                                                                                               linear
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36.00
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75.00%
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87.50%
77.08%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA POLYMERASE OF GAMMA HERPES VIRUSES
ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
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Indels:
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                             Conservative: Mismatches:
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   Gaps:
                Indels:
                                                            Matches:
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RESULT 15
US-09-221-017B-38/c
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                  Score:
                                                                                 Alignment Scores
                                                                                                                   US-09-221-017B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Application US/09221017B Patent No. 6444799
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                  .
No.:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MONTOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSS, Bruce C. TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 686 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PP15
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     ORIGINAL SOURCE
                                                                                                                                                                                                                                 MOLECULE TYPE: DN
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TEX: 706141
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                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 755 PAGE CITY: Palo Alto
                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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               Conservative: Mismatches:
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DB: 4 Gaps: 0
US-10-008-355-26 (1-9) x US-09-221-017B-38 (1-686)

QY 1 ThrGlyGlyAsnSerGlySerProVal 9
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Db 482 ACGGGCGGATCATCCGCTTCCCCGATC 456

Search completed: December 20, 2002, 14:11:52
Job time: 36.5789 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-Cgn2_1/USPTO_spool/US10008355/runat_17122002_112339_14635/app_query.fasta_1.398
-Q-/Cgn2_1/USPTO_spool/US10008355/runat_17122002_112339_14635/app_query.fasta_1.398
-DB=Published_Applications_NA -QEMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANKS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THP_MAX=100
-THR_MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10008355_@CGN 1_1_21_@runat_17122002_112339_14635
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPOP=10 -SDELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                            Result
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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85.4
83.3
83.3
                                                                                                      Match Length DB
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                                                                                                                                                                                                                                                                                       : /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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3: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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  US-10-008-355-1
0 US-09-070-927A-261
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7.0
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99.214 Million cell updates/sec
Sequence 1, Appli
Sequence 261, App
Sequence 1705, Ap
Sequence 243, App
                                                                                                      Description
                                                             Score:
                                                                                                      Alignment
                                                                                  Pred. No.:
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5174 520 557 765 2000 2000 2155 2155 2191 2191 2191 2192 2114 2174 2370 2370 2764 2764 2764 2764 2764 2764 2764 2764	1775 454 491 1114 400
100010000000000000000000000000000000000	10010
09-974-300-327 09-974-300-327 09-815-242-8179 99-938-842A-305 99-938-842A-30 99-938-842A-30 99-938-946-761-2449 90-960-352-9622 90-960-352-9622 90-960-352-303-55 90-912-363-38 90-912-363-38 90-918-326-131 90-718-276-21 90-718-276-21 90-718-276-21 90-764-869-1943 90-764-869-1943 90-764-869-1943 90-815-343-1415 90-815-343-1415 90-815-343-1415 90-815-343-1415 90-815-343-1415 90-815-343-1415 90-815-343-1415 90-815-343-676 90-815-343-676 90-815-343-676 90-815-343-676 90-815-343-676 90-815-343-676	10-001-887-75 -09-770-444-59 -09-783-590-65 -09-808-701-14 -09-960-352-14
	quence 75, Applequence 591, Apequence 591, Apequence 14, Appequence 14943,

ALIGNMENTS

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Best Local Similarity:
Query Match:
                                                                                                                    US-10-008-355-1
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-008-355-1
                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of
FILE REFERENCE: 235.00440101
                                                                                                                                                                  SOFTWARE: Patentin
SEQ ID NO 1
LENGTH: 2139
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10008355
Patent No. US20020164759A1
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
                                                                                                                                 ORGANISM: Porphyromonas
                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                     version
 4.69
48.00
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               Matches:
Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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   US-09-867-701-1705
                                                                                                                               US-10-008-355-26 (1-9) x US-09-070-927A-261 (1-4951)
                                                                                                                                                                                                                                                                                                                       ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-070-927A-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-008-355-26 (1-9) x US-10-008-355-1 (1-2139)
                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 261, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 261: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                          1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Enterococcus NUMBER OF SEQUENCES: 982
                                                         ACCGGCGGTCAATCTGGTTCACCAATC 669
                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kenley K. Hoover REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4951 base pairs
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88.89%
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Matches:
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Indels:
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                   US-10-001-887-75
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; Sequence 75, Application US/10001887
                                      RESULT 5
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; SOFTWARE: PatentIn Ver. 2; SEQ ID NO 243; LENGTH: 7441
; TYPE: DNA; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-09-764-878-243/c
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                                                                   US-10-008-355-26 (1-9) x US-09-764-878-243 (1-7441)
                                                                                                                                        Percent Similarity:
Best Local Similarity:
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1705
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 243, Application US/09764878 Patent No. US20020090615A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                            Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (1)...(450)
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2023 GGCGGTAACACAGGCAGCCCTGTG 2000
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                  2 GlyGlyAsnSerGlySerProVal 9
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LENGTH: ACT NO. 1.2.

L. CLICANT: HOFfman, Neil
L. CLICANT: HUEDAN, Neil
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for ""
LENGTH: "
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and FILE REFERENCE: DEX-0269
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Cafferkey, Robert
Sun, Yongming
Liu, Chenghua
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Hamilton, Carol M.
Price, Jennifer L.
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Ledford, Brooke L.
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Haas, William David
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Rameaka, Joshua G
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Percent Similarity:
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Query Match:
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LENGTH: 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT FILING DATE: 1000-02-15
PRIOR APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
PRIOR PRIOR APPLICATION NUMBER: 08/346,731
PRIOR PRIOR DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 11485
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                       LOCATION: (428)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (356)
OTHER INFORMATION: n equals a,t,g,
                   OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (463)
                                                                                                                                                  LOCATION: (421)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g, or c
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o. US20020110850A1
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RESULT 9
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Best Local Similarity:
Query Match:
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Query Match:
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Sequence 14943, Application US/09960352 Patent No. US20020137139A1
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
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APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: pt_FL_genes Version 2.0 SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Rui-hong
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20020146757A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2D
FILE REFERENCE: 790CIP2D
CURRENT APPLICATION NUMBER: US/09/808,701
CURRENT FILING DATE: 2001-03-14
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
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LOCATION: (131)..(952)
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Chen, Rui-hong
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Indels:
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GENERAL INFORMATION.

GENERAL INFORMATION G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTIVED OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 09/632,366
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; ORGANISM: Bos taurus
; OTHER INFORMATION: C:
US-09-960-352-14943
                                             PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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LENGTH: 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: PCT/US01/00662 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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; OTHER INFORMATION:
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US-09-864-761-32393
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                                                 US-10-008-355-26 (1-9) x US-09-974-300-327 (1-534)
                                                                                                  Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                      ; ORGANISM: Bacillus licheniformis US-09-974-300-327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 32393
LENGTH: 222
                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 327
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 327, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
DRIOR APPLICATION NUMBER: 09/680,598
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PRIOR
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PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                     No.:
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-0: APPLICATION NUMBER: FILING DATE: 2001-0:
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              GlyGlyAsnSerGlySerProVal 9
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2001-01-30
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37.00
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EXPRESSED IN LUNG,
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Matches:
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RESULT 12
US-09-864-761-15889/c
; Sequence 15889, Application
; Sequence US20020048763A1
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US-10-008-355-26 (1-9) x US-09-864-761-15889 (1-557)
                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                          ; OTHER INFORMATION: ; OTHER INFORMATION: US-09-864-761-15889
                                                               Query Match:
                                                                                                                              Score:
                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Annomax
SEQ ID NO 15889
LENGTH: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSTS BY .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                  No.:
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APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                  Conservative: Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Staphylococcus
US-09-815-242-4296
                                                                                                                                                                                                                 RESULT 14
US-09-815-242-8179
Sequence 8179, Application US/09815242
Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4296
LENGTH: 720
                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                       APPLICANT:
                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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                                                                                                                                                                                                                                                                                                                      167
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Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3053
LENGTH: 2000
                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-09-938-842A-3053
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Best Local Similarity:
Query Match:
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                                                                              Alignment Scores:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Percent Similarity:
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 8179
LENGTH: 765
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END--1 -MATRIX=bicsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIXE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10008355_@CGN_11_10_@funat_17122002_112336_14573 -NCPU-6 -ICPU=3
-NO_XLPXY -NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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-MODEL=frame+_p2n.model -DEV=xlh
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SUMMARIES

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AAS59888 ABL22883 AAS59845 AAH68579 AAK70665 AAK70664 AAV80633 AAH14840 ABL22872	AAL17622 AAL00017 AAC27896 ABL93826 AAN80912 AAA07168	ABC54166 ABT03070 AAC59942 AAH33087 ABA96872 ABL06881	AAS20000 AAF79971 ABV56742 AAF14488 ABK32891 AAX04382 AAF626291	AAX20213 ABN98198 AAX20212 ABN98197 ABQ91212 ABX13198 ABX13198 ABL7536 AAX29979	AAV75063 AAQ27988 AAQ27987 AAL43635 AAH52485 ABN91429 AAH543330	ID
Human novel cytoki Drosophila melanog Human novel cytoki Human protein HP10 Human immune/haema Human immune/haema Kidney injury asso Human cDNA sequenc Drosophila melanog	Human breast cance Human reproductive Human secreted pro Arabidopsis thalia Sequence encoding Pig lung protease	Human ovarian anti Human breast speci Human secreted pro Human colon cancer Human flavoprotein Drosophila melanog	coding I	111 111 111 111 111 111 111 111 111 11	rom rom rom nas idi	Description

ALIGNMENTS

AAV75063 RESULT 1 Staphylococcus aureus Staphylococcus aureus contig SEQ ID #752. AAV75063; AAV75063 standard; 16-MAR-1999 (first entry) DNA; 1019

Key Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds. Location/Qualifiers

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US-10-008-355-26
                                                                                                                                                                                                                                                                    Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.
                                                                                                                         71LT 2
7988
                                                                                                                                                                                                                                                                                     Local Similarity:
                   Protease from S. Aureus
                                               11-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1646-1647; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide(s) and proteins derived stored on computer readable medium and anti-S.aureus vaccines
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                                                                            AAQ27988;
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                                                                                                        AAQ27988 standard;
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                                                                                                                                                                                                                                                                                                                  1050
   mat_peptide
                             sig_peptide
                                                                                                      Staphylococcus
                                                                                                                                                                                              11-FEB-1993
                                                                                                                                                                                                                                                        AAQ27987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 15-16; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid residues in polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protease prepd. using Bacillus or Saccharomyces host - capable of cleaving peptide bond at carboxyl terminus of glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP04211370-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
                                                                                                                                  Protease; PCR;
                                                                                                                                                               Protease from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR29644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-304938/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease; PCR; amplify;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B₽;
                                                                                                                                                               S. Aureus ATCC12600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aureus
                                                                                                      aureus.
                                                                                                                                  amplify;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91JP-0024633
                             /*tag= & 352..555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
558..1361
/*tag= c
/*tag= b
556..1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7*tag= 2
                                                          Location/Qualifiers 352..1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 354..1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      579 A; 282 C;
                                                                                                                                                                                                                                                                                                                                                                                                   33.8
48.00
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                                                                                                                                                                                                                                                      DNA;
                                                                                                                                  Staphylococcus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                           AAL43635
                                                                                                                                                                                                                                                                                                                                        RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                         US-10-008-355-26 (1-9) x AAQ27987 (1-1586)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAQ27987-88 encode proteases which were isolated from Staphylococcus aureus strains. The DNA sequences were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protease prepd. using Bacillus or Saccharomyces capable of cleaving peptide bond at carboxyl terminus acid residues in polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP04211370-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-304938/37.
P-PSDB; AAR26842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1992.
                                                                                                                                                                                                          Dipeptidylpeptidase-7; DPP-7; go DPP-7 inhibitor identification;
                                                                                                                                                                                                                                                                    05-SEP-2002
                                                                                                                                                                                                                                                                                                                AAL43635 standard; DNA; 2139
                                                                                                                                                                                                                                                                                                                                                            1048 ACTGGTGGTAACTCAGGTTCACCAGTA 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1586 BP; 590 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 13-15; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1991;
(UYGE-) UNIV GEORGIA RES FOUND INC.
                     08-NOV-2000; 2000US-246827P
                                            08-NOV-2001; 2001WO-US46782
                                                                   16-MAY-2002.
                                                                                          WO200238742-A2
                                                                                                                                                                       Porphyromonas gingivalis
                                                                                                                                                                                               periodontitis,
                                                                                                                                                                                                                                         Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHIO ) SHIONOGI & CO
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...
                                                                                                                                                                                                                                                                                                                                                                         1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0024633
                                                                                                             /*tag= a
/product= "Porphyromonas gingivalis DPP-7"
                                                                                                                                                Location/Qualifiers
                                                                                                                                        .2139
                                                                                                                                                                                                                                                                                                                                                                                                                                  34.4
48.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 C;
                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                       gene; ds; enzyme; amidolytic cleavage;
n; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 G; 475 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                               1586
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of glutamic
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Best Local S:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-008-355-26 (1-9) x AAL43635 (1-2139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequence of the porphyromonas gingivalis dipeptidylepetidase, 7 (ppp-7) enzyme. The ppp-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The ppp-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The ppp-1 protein and DNA sequences of the invention are useful for identifying a ppp-7 inhibitor. ppp-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present DNA sequence encodes the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1930 ACGGGCGGTAACTCCGGTAGCCCCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
Nucleic acids encoding useful for vaccinating
                                           WPI; 2001-316495/33.
P-PSDB; AAG81635.
                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                         03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 4; 65pp;
                                                                                         Kimmerly WJ;
                                                                                                                                                  09-NOV-1999;
                                                                                                                                                                             09-NOV-2000;
                                                                                                                                                                                                                                                                    Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                            S. epidermidis open reading frame nucleotide sequence SEQ ID NO:363
                                                                                                                                                                                                                                                                                                                                                                                                       AAH52485;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH52485 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2139 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Travis J,
                                                                                                                                                                                                            17-MAY-2001
                                                                                                                                                                                                                                        WO200134809-A2
                                                                                                                      (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-490075/52.
DB; AAO15205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potempa JS,
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                               2000WO-US30782
                                                                                                                                                   99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 A; 543 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.3
48.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -  \begin{tabular}{ll} \end{tabular} \label{eq:condition}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  849
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                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1956
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Matches:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487 T; 0 other;
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ABN91429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC (II) given in AAG81454 to AAG83120, from Staphylococcus epidemics (II) can have antibacterial activity and therefore can be used CC (I) and (II) can have antibacterial activity and therefore can be used CC in vaccination. The nucleic acids (I) may be used to produce the CC S. epidermidis polypeptides (II) van the production of vectors CC containing them which are used to produce hosts cells which express the CC used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their CC crivity and therefore identify compounds that may be used for the CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to CC AAH55090 represent specifically claimed S. epidermidis genomic DNA CC polynucleotide sequences from the present invention. AAH55091 to CC AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

CC N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even considered the present invention are given in the disclosure for SEQ ID NO:4465 to 4472, the polynucleotide sequences are given in the disclosure for SEQ ID NO:4465 to 4472, the polynucleotide sequences are given in the disclosure for SEQ ID NO:4465 to 4472, the polynucleotide sequences are given in the disclosure for SEQ ID NO:4465 to 4472, the polynucleotide sequence is the polynucleotide sequence is the present property of the present specification, the polynucleotide sequence is the present property of the present specification, the polynucleotide sequence is the present property of the present specification, the polynucleotide sequence is the present property of the present specification of the present property of the present specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                      14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus antibacterial;
                                                             P-PSDB;
                                                                                                                         Doucette-Stamm
                                                                                                                                                                                                                                                                 13-AUG-1998;
                                                                                                                                                                                                                                                                                                       30-APR-2002
                                                                                                                                                                                                                                                                                                                                              US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                     StaphyLococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN91429 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-381255/41.
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                                                               ABP38884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 138-139; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH53970 represent nucleic acids (I) encoding polypeptides in AAG81454 to AAG83120, from Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        epidermidis; open reading frame; ORF; bacterial infection; gene therapy; gene; ds.
                                                                                                                       LA,
                                                                                                                                                                                                                                                                                                                                                                                   epidermidis
                                                                                                                                                                                                      97US-055779P.
97US-064964P.
                                                                                                                                                                                                                                                               98US-0134001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 A; 122 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137
43.00
100.00%
100.00%
89.58%
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                 The stand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
              in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express polypeptides. The polypeptides (II) (and/or nucleic acids) may then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frame (ORP) nucleic acid sequences which encode the amino acid sequency given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infection particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.
polypeptides. The polypeptides (II) (and/or nucleicused to vaccinate subjects and to raise antibodies
                                                                        AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used
                                                                                                                                                                  Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                       Claim
                                                                                                                                                                                                                                              Kimmerly WJ.
                                                                                                                                                                                                                                                                                                          09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                        09-NOV-2000; 2000WO-US30782
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH54330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH54330 standard; DNA; 3189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN90538 to ABN93374 represent Staphylococcus epidermidis open frame (ORF) nucleic acid sequences which encode the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD
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                                                                                                                                      Page 1307-1308; 2188pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             us epidermidis SR1 strain; endocarditis; ds.
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06-MAY-1997;
16-MAY-1997;
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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472.
                                                                                               genes,
                                                                                                                                                                                                                                                           New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bailey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection;
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The present sequence encodes an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attenuation;
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                                                                        The present invention provides the protein and coding sequences of a number of polypeptides from Entercocccus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Entercocccus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis
                                                                The polynuclinfection. T
                                           Sequence
                                                                                                                                             Claim 1; Page 197-198;
                                                                                                                                                                           New genes and polypeptides from Enterococcus faecalis, useful vaccines for preventing, treating or attenuating an infection a member of the Enterococcus genus in an animal, particularly
                                                                                                                                                                                                                        WPI; 2002-425450/45.
P-PSDB; ABP43442.
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                                                               The present sequence is a coding
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                                               US-10-008-355-26 (1-9)
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                                                                  Query Match:
DB:
                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                          Alignment Scores:
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                       sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screer compounds to identify agonists and antagonists of E. faecalis products.
                                                                                                                                                                                                  The present sequence represents a gene isolated from Enterococcus faecalis. The present invention describes genes, proteins can and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide
                                                                                                                                                                                                                                                                     Claim 1; Page 212; 301pp; English.
                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis; i
detection; attenuation;
                                                                                                                                             Sequence 888 BP;
                                                                                                                                                                                                                                                                                                                                                          Bailey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9850554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX20212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX20212 standard;
                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                No . :
          703
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                            μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThrGlyGlyAsnSerGlySerProVal 9
                           ThrGlyGlyAsnSerGlySerProVal 9
          ACCGGCGGTCAATCTGGTTCACCAATC 729
                                                                                                                                                                                                                                                                                                                                        1999-070095/06.
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                                                                                                                                                                                                                                                                                                                               AAY00222
                                                                                                                                                                                                                                                                                                                                                          Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           faecalis
                                                                                                                                                                                                                                                                                                                                                                                              97US-0066009.
97US-0044031.
97US-0046655.
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41.00
88.89%
77.78%
85.42%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene EF110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection;
                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigenic; ss.
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                                              (1-888)
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                                                                                                                                                                                                                                                                                                                                                          ۸,
                                                                                                                                             186 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                                                    Conservative: Mismatches:
                                                                  Gaps:
                                                                                                        Matches:
                                                                            Indels:
                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                          Kunsch
                                                                                                                                             253 T;
                                                                                                                                                                                                                                                                                                                                                          CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response;
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                                                                                                                                             other;
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                                                                                                                                                                                                                                                                                                           used to develop
                                                                                                                                                                                   for screening
                                                                                                                                                                                                                                                                                                  vaccines
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                                                                                                                                                                        protein
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ABN98197
ID ABN98
XX ABN98
XX ABN98
XX ABN98
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KW Enter
KW Gene;
XX Enter
XX Enter
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XX US200
XX US200
RESULT 12
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Query Match:
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                                                                                                       ABQ91212/c
                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                      vaccines
a member
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 200
P-PSDB;
                                    M. capsulatus
                                                       01-OCT-2002
                                                                           ABQ91212;
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN98197;
                                                                                             ABQ91212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002045737-A1
                                                                                                                                                                                                                                                                                                                                                                             faecalis
                                                                                                                                                                                                                                          No..
                                                                                                                                                                                                                                                                     888
                                                                                                                                                                                                                                                                     BP;
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US-10-008-355-26 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis.
Methylococcus capsulatus
                                    Micro array; gene; ds; differential expression; gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E faecalis EF110 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN98197 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes and polypeptides from Enterococcus faecalis, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis
                                                                                                                                                                                                                                                               703 ACCGGCGGTCAATCTGGTTCACCAATC 729
                                                                                                                                                                                                                                                                                           ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-425450/45
DB; ABP43441.
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for preventing, treating or attenuating an infection of the Enterococcus genus in an animal, particularly
                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bailey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a coding sequence of
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0071035
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                                                                                                                                                                                                                                                                                                                                    x ABN98197 (1-888)
                                                                                                                                                                                                                                                                                                                                                                        326
41.00
88.89%
77.78%
85.42%
                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255pp;
                                                                      #1197 for DNA array.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastrointestinal disease; diagnosis; antibiotic;
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                                                                                                                                                                                      2130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 G; 253 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
14-NOV-1997;
06-MAY-1997;
                                                                                                                                                                                                                                                               1661 ACCGGCGGCAACGCTGGCTCGCCG 1638
                                04-MAY-1998;
                                                                                                Enterococcus
                                                                                                                               Enterococcus faecalis;
                                                                                                                                                     Enterococcus
                                                                                                                                                                            19-MAR-1999
                                                                                                                                                                                                  AAX13198;
                                                                                                                                                                                                                     AAX13198 standard; DNA; 4951 BP
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 497; 678pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capsulatus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-557818/59.
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                                                                            WO9850555-A2
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Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-2002; 2002WO-NO00019
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                                                      12-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              THYENCION.
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12-JAN-2001; 2001NO-0000239;
                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                                                     1 ThrGlyGlyAsnSerGlySerPro 8
                                                                                                                      attenuation;
                                                                                                                                                                          (first entry)
                                                                                                                                                     faecalis
                                                                                                 faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
97US-0066009
97US-0044031
                                98WO-US08985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lossius I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eidhammer I,
                                                                                                                                                                                                                                                                                                            x ABQ91212
                                                                                                                                                                                                                                                                                                                                                                                                                       363 A;
                                                                                                                                                                                                                                                                                                                                  824
41.00
100.00%
87.50%
85.42%
24
                                                                                                                                                     genome
                                                                                                                    computer readable medium;
                                                                                                                               contig;
                                                                                                                                                                                                                                                                                                                                                                                                                         633
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                                                                                                                                                   contig SEQ
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                                                                                                                                                                                                                                                                                                            (1-2130)
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isen JA, Fraser CM,
                                                                                                                               detection; Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                       705
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                       429
                                                                                                                                                     ID NO:261
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                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
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DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for disposing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
WPI; 2002-122075/16
                                                                                                                                                                                                                                                      Human ovarian cancer related cDNA clone SEQ ID NO:1705
                                                                                                                                                                                                                                                                                   17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAXI3938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                          Algate PA,
                                                                                                                                                                    WO200192581-A2
                                                                                                                                                                                                                            Human; ovarian
                                                                                                                                                                                                                                                                                                              ABL78727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4951 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1248-1251; 2084pp; English
                                                                                                             29-MAY-2001; 2001WO-US17756.
                                                                                                                                         06-DEC-2001
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          ABL78727 standard;
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                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection.
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                                                                                                                                                                                                                                                                                                                                                                                                 695 ACCGGCGGTCAATCTGGTTCACCAATC 669
                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scores:
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                          Harlocker
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                                                                                 2000US-207484P
                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                        cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0046655
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41.00
88.89%
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                                                                                                                                                                                                                                                                                                                                          cDNA; 450
                                                                                                                                                                                                                                                                                  entry)
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                          Jones
                                                                                                                                                                                                                                                                                                                                          ВP
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
(NOVO ) NOVO NORDISK BIOTECH INC
                                                   22-MAR-1999;
                                                                                                                                                                                                                                                                                           expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reese; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF07536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -
                                                                                               22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                    WO200056762-A2
                                                                                                                                                                                                                                                  Fusarium venenatum
                                                                                                                                                                                                                                                                                                                                                                                                Multiple gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium venenatum EST SEQ ID NO:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF07536 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a CDNA sequence (SI) from the 10912 nucleotide sequences as given in ABL77023 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 1705; 489pp; English
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Sequence 1127

BP;

232 A; 356 C; 268 G; 258 T; 13 other;

present invention.

specifically claimed in the

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the global expression of genes from FF cells allows the production continuous to be improved. New genes may be conditioned in the microorganisms to be improved. New genes may be conditioned. The obsible functions of unknown open reading frames can be conditioned. The expression of genes can be used to study how FF cells cadapt to changes in culture conditions, environmental stress, spore compined to changes in culture conditions, environmental stress, spore compined to change in culture conditions, environmental stress, spore compined to change including chain atton of redundancy as one spot on an analysis of constitution of including frame, and organisation of the carray equals one gene or open reading frame, and organisation of the carray equals one gene or open reading frame, and organisation of the carray equals one gene or open reading frame, and organisation of the carray equals one gene or open reading frame. The presents ESTs from Aspergillus oryvae; and carray shafills to AAF11878 to AAF11873 represents ESTs from Aspergillus oryvae; and call to confirm the present set of the carray carray and call to confirm the present of the carray car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monitoring differential expression of genes uses fluorescence-labeled nucleic acids isol substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86; Page 393-394; 3161pp; English.
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cells and a
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Дb Ş US-10-008-355-26 (1-9) x AAF07536 (1-1127) Query Match: Best Local Similarity: Alignment Scores: Percent Similarity: 332 No . : 2 GlyGlyAsnSerGlySerProVal 9 GGAGGGAACTCAGGAACACCAGTG 632 40.00 100.00% 87.50% 83.33% 21 309 Indels: Mismatches: Matches: Conservative: 1127 7 1 0 0 0

Search completed: December 20, 2002, 13:22:54 Job time : 175.474 secs

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US-09-071-035-428
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AT TO MENERO	PCT-US95-06266-89	US-08-485-910-106	US-08-461-361-106	US-08-464-134-106	US-08-444-733-106	US-08-466-033-106	US-08-817-787-17	US-08-946-026-5	US-08-638-911A-8	US-08-483-432-23	US-08-479-939-23	us-08-361-920-23	US-08-887-365-36	US-09-219-849-38	us-08-976-161-69	US-08-450-945-69	US-08-969-630-2	US-08-969-630-4
	Sequence 89, Appl	Sequence 106, App	•	-	-	Sequence 106, App	Sequence 17, Appl	Sequence 5, Appli	Sequence 8, Appli	Sequence 23, Appl	•	•	`	Sequence 38, Appl	`	Sequence 69, Appl	Sequence 2, Appli	Sequence 4, Appli

ALIGNMENTS

Title:

US-08-332-562A-67 TELERAX: (202,0... TELEX: 904136 INFORMATION FOR SEQ ID NO: 67 SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids Sequence 67, Application Patent No. 5985599 PATENL NO. JOILE PATENL NO. PATENL NO. PATENLON: APPLICANT: MCKENZIE, Ian F.C. APPLICANT: HOGARTH, Mark P. APPLICANT: HIBBS, Margaret L. APPLICANT: SCOTT, Bernadette M. APPLICANT: SCOTT, Bernadette M. APPLICANT: SCOTT, BULL. APPLICANT: BONADONNA, Lisa APPLICANT: HULETT, Mark D. TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN TITLE OF INVENTENCES: 136 REFERENCE, DOCKET NUMBER: 54 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300 TELEFAX: (202)672-5399 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0' FILING DATE: 27-MAY-1992 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy APPLICATION NUMBER: US/08/332,562A FILING DATE: 31-OCT-1994 CLASSIFICATION: 435 STREET: 3000 K S CITY: Washington STATE: D.C. TYPE: amino acid STRANDEDNESS: sir NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 TOPOLOGY: COUNTRY: 20007-5109 E: Foley & Lardner 3000 K Street, N.W., USA linear Floppy disk single US/08332562A US 07/896,457 67: 54270/119/GRHA Suite 500

100.0%;

Score 48; DB 2; Pred. No. 0.083;

2;

Length 15;

Matches

9;

Conservative

0;

Mismatches

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Best Local Similarity
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                                                                                                                                                        RESULT 3
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; MOLECULE TYPE:
US-08-523-373-22
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US-08-523-379-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-238595

FILING DATE: 07-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-296028

FILING DATE: 07-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.

REGISTRATION NUMBER: 36,607
                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 22:
                                  APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
CORRESPONDENCE ADDRESS
                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                           165 TGGNSGSPV 173
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 213 amino acids TYPE: amino acid strandedness: not relevations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                      3) Application US/08523373
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6037145
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                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                  PROCESS FOR PRODUCTION OF PROTEIN
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                                                                                                                                                                                                                                                                                             Score 48; DB 3; Length 213; Pred. No. 1.1;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: JF 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY,AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 23:
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 TGGNSGSPV 173
                                  APPLICATION NUMBER: US/O FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22314-3187
                                                                                                                                                                                                                                        STREET: 699 Prince CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                             ADDRESSEE: BURNS, Jones, STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 05-SEP-1995
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CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08523373 6037145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
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                                                                        US/08/523,373
 JP 6-238595
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Pred. No. 1
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; MOLECULE TYPE: peptide
US-08-523-373-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-657-192-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08657192
Patent No. 5747321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative C
                                                      TELEFAX: (703) 836-2021
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
PRIGTH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 6-2
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MEULH, DONNA M.
REGISTRATION NUMBER: 36,60
 MOLECULE TYPE:
                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 TGGNSGSPV 173
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0: FILING DATE: 03-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
STATE: Virginia
                  TOPOLOGY:
                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OHSUYE, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YABUTA,
                  linear
                                                                                                                                      (703) 836-6620
protein
                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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                                                                                                                                                                         001560-264
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Pred. No. 1
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US-08-523-

GENERAL INFORMATION:

Application US/08523373 6037145

APPLICANT:

Yabuta, Masayuki Ohsuye, Kazuhiro

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В
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                                                                                          Query Match
Best Local Similarity
"~*~hes 9; Conserv?
                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-523-373-5
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RESULT 7
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                      TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                             289 TGGNSGSPV 297
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                                                                                                                                                                                                                                                                               TELEPHONE: 703 - TD NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 05-SEP CLASSIFICATION: 435
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ZIP: 22314-3187
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                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                    TYPE:
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                                                                           1 TGGNSGSPV 9
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100.0%; Pred. No. 1.8;
tive 0; Mismatches
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Pred. No. 1.8;
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                                                                                                                                     DB 3; Length 344;
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                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08657192
Patent No. 5747321
GENERAL INFORMATION:
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Best Local 9
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FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             APPLICANT: YABUTA, Masayuki
APPLICANT: OHSUYE, Kazuhiri
TITLE OF INVENTION: MUTANT S
TITLE OF INVENTION: PROTEASE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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APPLICATION NUMBER:
                                                                                                                                                             STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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TYPE: amino acid
STRANDEDNESS: not releva
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STATE: VA
                                                                                                                                              COUNTRY:
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Similarity 100.0%;
9; Conservative 0
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22313-1404
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US/08/657,192
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Pred. No.
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Best Local :
                                                               TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-238595

FILING DATE: 07-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-296028

FILING DATE: 07-NOV-1994
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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LENGTH: 532 amino acids
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                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
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                                                                                                                                NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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ZIP: 22314-3187
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STRANDEDNESS:
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                               532 amino acids
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not relevant
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Pred. No. 2
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RESULT 11
US-09-134-001C-3729,
Sequence 3729, Application US/09134001C
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US-08-657-192-15
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Matches
               GENERAL INFORMATION:
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                                                                                                                                                                                                         Query Match
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APPLICANT: Lynn Doucette-Stamm et al
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                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/657,192 FILLING DATE: 03-UN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YABUTA, Masayuki
APPLICANT: OHSUYE, Kazuhiro
TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
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nes 9; Conser
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                              537 amino acids
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P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                           (703) 836-6620
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                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                       36,607
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                                                                                                                                                                                                                                                                                                                                                                                                         001560-264
                                                                                                                                                                           Score 48; DB 1
Pred. No. 2.8;
0; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                         DB 1; Length 537;
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Query Match
Best Local Similarity
Thehes 7; Conserv
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                                                                                US-09-071-035-428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3729
LENGTH: 311
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                            TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acid
                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 GGNSGSPV 268
                                                                                                             STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ver
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                             LENGTH:
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                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                               (301) 309-8512
               Conservative
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                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Genome Sciences, Inc
                                                                                                                                                                                                                            (301)
                                                                                                                                                             amino acids
                                                                                              protein
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                                                                                                                             single
                                                                                                                                                                                                                            309-8504
                              85.4%;
77.8%;
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Pred. No.
                              Score 41;
Pred. No.
               Mismatches
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                                DB 4;
17;
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                                            Length 252;
             Indels
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             0;
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             Gaps
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1 TGGNSGSPV 9

TGGQSGSPI 200

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GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Chromatin Associated Proteins
FILE REFERENCE: BB-1118
CURRENT APPLICATION NUMBER: US/09/342,653
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,841
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-071-035-426
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; MOLECULE TYPE:
US-09-071-035-426
                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                 Sequence 7, Application US/09342653 Patent No. 6306632
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Best Local :
                SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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INFORMATION FOR SEQ ID NO:
LENGTH: 418
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                             224 TGGQSGSPI 232
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CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: single
linear
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 284;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-342-653-7
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   В
                                                Query Match
Best Local Similarity
Thes 7; Conserve
                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-090-048-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-090-048-1
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Budtz, Peter
APPLICANT: Nielsen, Per M.
TITLE OF INVENTION: PROTEIN PREPARATIONS
                                                                                                                                                                                                                         TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/DK92/00036
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3396.214-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 GGNSGNPI 170
164 GGQSGSPV 171
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DK 199/91 FILING DATE: 06-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United ZIP: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                             TELEPHONE: 212-867-0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/090,048 FILING DATE: 16-JUL-1993
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                                                                                                                                                                               STRANDEDNESS:
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                                 2 GGNSGSPV
                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                            : 222 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: No. 5523237o No. 5523237disk of No. 5523237th America, Inc.
405 Lexington Avenue, 62nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
                                                                 Conservative
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                                                                                 77.1%;
87.5%;
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75.0%;
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Pred. No. 57;
                                                                                 Score 37; DB Pred. No. 63;
                                                                  Mismatches
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                                                                                             Length 222;
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                                                                  Indels
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Search completed: December 20, Job time : 16.6316 secs

2002, 12:12:19

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Command line parameters:

-MODEL-frame+p2n.model -DEV=xlh
-O-/Ggn2_1/USPTO_Spool_VS10008355/runat_17122002_112338_14609/app_query.fasta_1.398
-DB=EST -OFMT-fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER-US10008355_eCGN_1_1_763_erunat_17122002_112338_14609 -NOPU=6 -ICPO=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , X
Fgapop 6.0 , E
Delop 6.0 , E
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BLOSUM62
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first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Z	REFERENCE 1 (bases 1 to 318)
EST.	AA411980.1 G1:20/0052 EST. human human Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo

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                                                                                    Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. au Direct Submission of BAC-end sequences from Anopheles Unpublished (2001)
                                                                                                                                                        Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                               BH400391
426 bp DNA linear GSS 11-DEC-200
AG-ND-147H4 TF ND-TAM Anopheles gambiae genomic clone AG-ND-147H4,
DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2072 Std Error: 0.00
                                                                                                                                                                                                                                         BH400391.1 GI:17346607 GSS.
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                               Contact: Brendan J Loftus
Department of Eukaryotic Genomics
                                                                    Other_GSSs: AG-ND-147H4.TR
                                                                                                                                                                                                                                                                          ВН40039
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Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 306.
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Fax: 314 286 1810
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                                                                                                                                                                                                                       African malaria mosquito
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                 Institute for Genomic Research
 Medical Center
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1 72 c
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/clone="IMAGE:727252"
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/db_xref="GDB:5924164"
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                  Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                           High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seati Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ699991 371 bp DNA linear HS_5334_A2_GO4_SP6E RPCI-11 Human Male BAC Library genomic clone Plate=910 Col=8 Row=M, DNA sequence.
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This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University, College Station, Texas 77843-2123, USA using a HindIII matter that the gut are the station of DNA from the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
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http://www.htsc.washington.edu
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/clone="AG-ND-147H4"
/clone_lib="ND-TAM"
/note="Vector: pEcBaC1; S
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/strain="PEST"
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g,J., Zhao,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                 High quality sequence stop: 677.
Location/Qualifiers
                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10682 row: 1 column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BG714149.1 GI:13993080
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a 88 c 79 g 117 t
/note="Organ: brain; Vector: pBluescriptk (modified pBluescript KS+); Site_1: BamHI; Site_2: Sal1-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="Plate=910 Col=8 Row=M"
/clone_lib_"RPCI-11 Human Male BAC Library"
                                                                                                     /clone="IMAGE:4797094"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Zea mays
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Contact: Walbot V
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1 (bases 1 to 279)
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
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Maize ESTs from various
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                                                                                                  61
                                                                                                                                                 /tissue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
: Site_2: EcoRI: Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illhois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     walbot@stanford.edu
687001 row: G colu
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                                                                                                1890s era
a 78 c
                                                                                                  concentration for 90 generations and originates from the 1890s era open pollinated variety Burr's White" 78 c 68 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free the IMAGE Consortium (info@image.llnl.gov) Insert Length: 389 Std Error: 0.00 Seq.primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 420)
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W72307.1 GI:1382930
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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Location/Qualifiers
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NbHL19W."
121 c 88 g 79 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:1270461"
/db_xref="taxon:9606"
/clone="IMAGE:345086"
                                                                                                                                                                                                                                                                                                                                                                                                /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_fetal_heart_NbHH19W"
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AGENCOURT_8728373 NIH_MGC_47
5', mRNA sequence.
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1 (bases 1 to 768)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
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602819216F1 NCI_CGAP_Mam6
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Plate: LLAM10899 row: o column: 04
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                                                                                                                                                                                                                                                                                                                                                                          /note="organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 206 c 203 g 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_fupe="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:4948443"
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                                                 EST 16-AUG-2002
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BE794754/c
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 970)
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                                                                                                                                                                                                                                                                          mRNA sequence.
BE794754
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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/lab_host="PM10B (phage-resistant)"
/lab_host="PM10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/clone="IMAGE:6339187"
/clone_lib="NIH_MGC_47"
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                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                          found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11652 row: e column: 11
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                               quality sequence start: 71 quality sequence stop: 136.
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/clone="IMAGE:3944516"
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                                           Location/Qualifiers
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/tissue_type="small cell carcinoma"
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                   correct orientation)
Seq primer: -40RP fr
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                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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IMAGE:722944 5', mRNA sequence.
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Location/Qualifiers
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                       /organism="Mus musculus
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:722944"
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/clone_lib="NIH_MGC_95"
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/lab_host="DH10B"
clone_lib="Soares mouse lymph node NbMLN"
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RESULT 12
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martln,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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AA242434
                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                       Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 337.
                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was primed with a Not I - oligo(dT) primer (5')
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                                                                   /clone_lib="Soares mouse
/tissue_type="Liver"
/lab_host="DH10B"
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                  /clone="IMAGE:681330"
                                                                                                                                                    /db_xref="taxon:10090"
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The WashU-NCI Mouse EST Project 1999
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mx26c10.x1 Soares mouse
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
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Bonaldo.
a 103 (
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92 c
                                                     double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                               /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:681330"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Other_ESTs: va14q09.yl
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 426)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800 Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
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                                                                                                      129
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                                                                                                 provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo." a 107 c \cdot 72 g 117 t 1 others
                                                                                                                                                          3']; double-stranded cDNA was ligated to Eco RI adapt (Pharmacia), digested with Not I and cloned into the and Eco RI sites of the modified pT7T3 vector. RNA
                                                                                                                                                                                                                                                     /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="lymph node"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:722944"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                /sex="male"
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                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse lymph node NbMLN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
Oligo-dT track served to identify it as a clone from the normalized
adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
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UI-R-CO-gw-c-07-0-UI.sl UI-R-CO Rattus norvegicus cDNA clone
UI-R-CO-gw-c-07-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Program for Rat Gene Discovery and Mapping University of Iowa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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               /lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: p7773D-Pac (Pharmacia) with a modified
/note="Vector: p7773D-Pac 
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/db_xref="taxon:10116"
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pooled UI-R-Al and UI-R-El library in the form
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Search completed: December 20, 2002, 15:49:00 Job time: 1377.95 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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SUMMARIES

344 18	344 17 AAR91033	336 13 AAR29644	100.0 215 17 AAR91044	214 17	100.0 213 17	52 23	52 23	10 23	1 48 100.0 9 23 AAO15229	No. Score Match Length DB ID	
Protein encoded by	Beta-galactosidase	Protease from S. A	V8 mature protease	V8 mature protease	V8 mature protease	Staphylococcus aur	Porphyromonas ging	Porphyromonas ging	Porphyromonas ging	Description	

ALIGNMENTS

RESULT 1 AAO15229 05-SEP-2002 AA015229; AAO15229 standard; Peptide; 9 Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) active site 2. (first entry)

Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; active site; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis

Porphyromonas gingivalis.

WO200238742-A2.

16-MAY-2002.

08-NOV-2001; 2001WO-US46782.

08-NOV-2000; 2000US-246827P.

(UYGE-) UNIV GEORGIA RES FOUND INC.

Potempa JS, Banbula A, Bugno

WPI; 2002-490075/52.

Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis $\,$

The

Claim

4;

Page

32;

65pp; English the

amino

acid and coding sequence of the ylpeptidase-7 (DPP-7) enzyme. The

The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents an active site region of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7)

Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.

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The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful reducing the growth of a bacterium and protecting an animal from a
                                                                       The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme between the enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.
                                                                                                                                                 Claim
                                                                                                                                                                       Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis \,
                                                                                                                                                                                                                                                               Travis J,
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DPP-7 inhibitor identification;
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                                                                                                                                                                                                                                                               Potempa JS,
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                                                                                                                                               The invention comprises the amino acid and coding sequence of the PP-7 Porphyromonas gingivalis dipeptidylpeptidase-7 (PPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a reducing the growth of a bacterium and protecting an animal from a
                                                                                                      or periodontitis).
C-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; qindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       periodontal disease caused by Porphyromonas gingivalls (e.g. gingivitis or periodontitis). The present amino acid sequence represents an active site region of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7)
                                                             Sequence
                                                                                                      periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Porphyromonas gingivalis dipeptidylpeptidase-7
                                                                                                                                                                                                                                                                                                                                               Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal
                                                                                                                                                                                                                                                                                                                                                                                                                         Travis J,
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                                                                                                                                                                                                                                                                                                    Example 6;
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-490075/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYGE-) UNIV GEORGIA RES FOUND
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9; Conser
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                                                                                                                                                                                                                                                                                                    Fig 5;
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100.0%; ilarity 100.0%; Conservative
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                                                             ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis dipeptidylpeptidase-7 (DPP-7) C-terminal region
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               Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                         A,
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0.27;
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                                23;
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                              Length 52;
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RESULT 5
AAR91042
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AAO15207
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    DEX DXX XX
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                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis;
V8 mature protease (aa1-213).
                             23-MAY-1996
                                                         AAR91042;
                                                                                   AAR91042 standard; Peptide;
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Fig 5;
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                                                                                                                                                                                                                                                                    52 AA;
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                           (first entry)
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Pred. No. 1.4;
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RESULT 6
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Best Local Similarity
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AAR91043;

33-MAY-1996 (first en+----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 molety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodn. of recombinant polypeptide(s) – using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                           Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
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07-SEP-1994;
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                        13-MAR-1996
                                                                          EP700995-A2
                                                                                                                            Staphylococcus
                                                                                                                                                                                                                                                                                                              V8 mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 TGGNSGSPV 173
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                                                                                                                            aureus
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                                                                                                                                                                                                                                                                                                                 (aa1-214).
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Pred. No.
                                                                                                                            (ATCC 27733)
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Prodn. of recombinant polypeptide(s) - using host cells transformed
                                                     Ohsuye K,
                                                                                                         07-NOV-1994;
07-SEP-1994;
                                                                                                                                                06-SEP-1995;
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                                                                                                                                                                                                                             Staphylococcus aureus strain V8
                                                                                                                                                                                                                                                    Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli, transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                           AAR91044;
                                                                                                                                                                                                                                                                                                                                                                                                    AAR91044 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Fig 14b; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of recombinant polypeptide(s) - using host cells transformed
with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-1995;
                                                                                                                                                                           13-MAR-1996
                                                                                                                                                                                                                                                                                                                      V8 mature protease (aa1-215).
                                                                                                                                                                                                                                                                                                                                                 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUNR ) SUNTORY LTD.
                                                                              (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    host cells.
                            1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGNSGSPV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100
9; Conservative
                                                     Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yabuta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 AA;
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                        94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94JP-0296028
94JP-0238595
                                                                                                                                                95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
Pred. No.
                                                                                                                                                                                                                           (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 8
AAR29644
ID AAR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
The sequences given in AAR26842 and AAR29644 are proteases which we isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                               Disclosure; Page 15-16; 25pp; Japanese
                                                                                                                         acid residues in polypeptide(s)
                                                                                                                                       Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of gl
                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                      03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR29644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR29644 standard; Protein; 336 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Fig 14c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                  20-FEB-1990;
                                                                                                                                                                                                                                                                           19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                JP04211370-A
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-1993
                                                                                                                                                                                                                      (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 TGGNSGSPV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGGNSGSPV 9
                                                                                                                                                                                              1992-304938/37
                                                                                                                                                                                AAQ27988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. Aureus
                                                                                                                                                                                                                                                  90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplify; Staphylococcus
                                                                                                                                                                                                                                                                           91JP-0024633
                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide
69..336
/label= Protease
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                       glutamic
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were

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RESULT 9
AAR91033
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                  δÃ
                             Query Match
Best Local Similarity
"~+~hes 9; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric
Chimeric
                                                                                                          Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pG97S4DhCT(G)R6, yielding pV8RFT(-) and pV8RFT(+), respectively. Both constructs yielded active protease
                                                                                                                                                                                                               Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                  Ohsuye
                                                                                                                                                                                                                                                                                                         07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                        06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-galactosidase-V8 protease fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR91033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91033 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                Sequence
                                                                                                                                                                                 Example 2; Page 12-13; 44pp; English.
                                                                                                                                                                                                                                              WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                 EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V8 protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1996
                                                                                                                                                                                                     polypeptide
                                                                                                                                                                                                                                                                                     (SUNR ) SUNTORY LTD
                                                                                                    when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TGGNSGSPV 9
                   1 TGGNSGSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGNSGSPV 241
TGGNSGSPV
                                                                                                  expressed
                                                                                                                                                                                                                                                                  ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tease; Staphylococcus aureus; recombinant
protein; beta-galactosidase; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli; Staphylococcus aureus strain V8 (ATCC 27733).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336
                                                                                                                                                                                                                                                                 Yabuta M;
                                                                                344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                    9
297
                                                                                                  in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                         94JP-0296028.
94JP-0238595.
                                                                                                                                                                                                                                                                                                                                        95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "beta-galactosidase region" 125..344
                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                             "mature V8 protease without the repeat
                                                                                                                                                                                                                                                                                                                                                                                                  region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                       0,
                                      Score 48; DE
Pred. No. 9.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB : Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                            DB
9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                         17;
                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 336;
                                                         Length 344;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                     Gaps
                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 10
AAW22218
                         Š
                                                                                                        В
                                                                                                                            The invention relates to new mutant Staphylococcus aureus V8 proteases Which have enzyme activity even under environmental conditions which promote protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K.

The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 48 amino acids linked, via a synthetic linker, downstream of the E. coli beta-galactosidase. The S. aureus portion of the chimaera was amplified by the priners AAT73254-5 from wild type sequence. The coding sequence was then used to generate mutants of the CV8 protease which retain their levels of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                Query Match
Best Local
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22218 standard; Protein;
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 13-14; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus V8 protease mutants -
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-013693/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22218
                                                                                                                                                                                                                                                                                                                                                                   resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP745669-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
289
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUNR ) SUNTORY LTD
                         1 TGGNSGSPV 9
TGGNSGSPV 297
                                                  Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                     Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                       344 AA;
                                                                                                                                                                                                                                                                                                                                                                   to denaturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity; fusion
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95JP-0170086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96EP-0303939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "E. coli beta-galactosidase
101..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "synthetic R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pV8RPT(-)
                                                              100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "truncated
                                                                .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344
                                                    0
                                                  Score 48; DB
Pred. No. 9.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aureus V8 protease portion'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-galactosidase;
                                                               DB
9.7;
                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                with increased
                                                    0
                                                                            Length 344;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        portion"
                                                    0;
                                                  Gaps
                                                    0;
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RESULT 11

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RESULT 12
AAR91034
  FH XXX
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                                                                                                                                                         δÃ
                                                                                                                                                                       Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                        The sequences given in AAR26842 and AAR29644 are proteases which we isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in
 Key
                Chimeric
                      Chimeric
                                             V8 protease;
                                                           Beta-galactosidase-V8
                                                                                         AAR91034;
                                                                                                       AAR91034 standard;
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                  Novel protease prepd. using Bacillus or Saccharomyces host - capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                         23-MAY-1996
                                                                                                                                                                                                                                                                     Disclosure; Page 13-15; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR26842 standard;
                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                       (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                                    19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                 JP04211370-A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR26842;
                                      fusion
                                                                                                                                                                                                                   polypeptide.
                                                                                                                                                                                                                                                                                                                                                      20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                           233
                                                                                                                                                                        Local Similarity es 9; Conserv
                                                                                                                                                   1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                 1992-304938/37.
DB; AAQ27987.
                                                                                                                                           TGGNSGSPV
                                    tease; Staphylococcus aureus;
protein; beta-galactosidase;
              Escherichia coli;.
Staphylococcus aureus strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR;
                                                                                                                                                                                                      357 AA;
                                                                                                                                                                        Conservative
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                      90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                    91JP-0024633
                                                                                                                                                                                                                                                                                                                                                                                                                                                           aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplify;
                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signal_peptide
69..358
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aureus ATCC12600.
                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                            100.0%;
                                                          protease fusion protein.
                                                                                                                                                                                                                                                                                                                                       LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus.
                                                                                                       392
                                                                                                                                                                        0;
                                                                                                                                                                       Score 48; DB Pred. No. 10; Mismatches
                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                    recombinant
Escherichia
               8
                                                                                                                                                                              10;
               (ATCC 27733).
                                                                                                                                                                                     13;
                                                                                                                                                                        0;
                                    coli.
                                                                                                                                                                                     Length 357;
                                                                                                                                                                        Indels
                                                                                                                                                                       0
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                        were
                                                                                                                                                                       0;
                                                                                                                                                                                     RESULT 13
AAR91035
밁
                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 9
                                                                Chimeric
Chimeric
      Cleavage-site
                                                          Chimeric
                                                                               Chimeric
                                                                                                                                                 23-MAY-1996
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-1994;
07-SEP-1994;
                    Region
                                   Region
                                                                                                                                                                              AAR91035
                                                                                                                                                                                                                                                                                        when expressed in E.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                            (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                  289 TGGNSGSPV 297
                                                                                                                                                                                                                                1 TGGNSGSPV 9
                                                                                                                                                                                                                                              l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                               Escherichia coli;
                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                            392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              Yabuta M;
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "b
125..392
      104..105
                      101..120
                                    1..100
/note=
                                                                                                                                                                              Protein;
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recombinant protein; fusion protein; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pG97S4DhCT(G)M6, Y1elding pV8RPT(-) and pV8RPT(+), respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                                                                                                  Linker peptide; V8 protease;
                                                                                                                                                                                                                                                                                                                                                                                             Recombinant V8 protease V8D fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 14-15; 44pp; English.
                                                                                                                                                                         synthetic;
Staphylococcus aureus
transposon Tn903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative
                                                                            /note= "beta-galactosidase
                                                                                                                            Location/Qualifiers
                                          /note= "R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mature V8 region"
"cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48;
Pred. No.
                                                                                                                                                                                             strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease
                                                                                                                                                                                                                                                                                                                              beta-galactosidase;
                                                                                                                                                                                                8٧
for OmpT protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                             (ATCC 27733);
                                                                                   region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 392;
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AAW22219
ID AAW
XX
AC AAW
XX
DT 11-:
DE Prol
XX
KW Muta
KW Prol
XX
KW Prol
XX
Chi
XX
Chi
XX
RE Reg:
FT Reg:
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                             Chimeric
Chimeric
                              Key
Region
 Region
                                                                                                                          proteolytic activity;
                                                                                                                                         Mutant; Staturncation;
                                                                                                                                                                                                                                                                              AAW22219 standard; Protein; 532 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respectively), B is Staphylococcus aureus mature v8 protease lacking the C-terminal repeat region, and L is a linker peptide (AAR91032). The fusion protein is expressed in inactive form in E. coli. It is then recovered, solubilised and cleaved at the linker peptide regions with a protease intrinsic to the host cells, i.e. OmpT protease, to allow recovery of V8 protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides (derived from Escherichia coli beta galactosidase and and Tn903 aminoglycoside 3' phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 16-18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1994;
07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                              TGGNSGSPV 297
                                                                                                                                                                                                                                                                                                                                                                                           TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conserv
                                                                                                                       Staphylococcus aureus; V8 protease; enzyme; denaturation; ion; wild type; PCR; polymerase chain reaction; amplificat. ytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                      encoded by pV8D construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yabuta M;
                                                                           Staphylococcus
                                                                                             Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "R6 linker"
339..340
/note= "cleavage site f
307..532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94JP-0296028.
94JP-0238595.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125..335
/note= "V8
336..356
              /note= "E. coli beta-galactosidase portion"
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                             coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "aminoglycoside 3'phosphotransferase
region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease region"
                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for OmpT protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 532;
                                                                                                                                    amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                RESULT 15
AAW22220
QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to new mutant Staphylococcus aureus V8 proteases which have enzyme activity even under environmental conditions which protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino cadds from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, W13 and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 56 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the V8 protease fragment is a second R6 linker and a fragment of the caminoglucoside 3' phosphotransferase protein. The chimaeric sequence was generated by restriction digestion and ligation from the V8RPT(-) sequence (see AAW22218) by using a natural EcoRV site which removed a further 8 amino acid from the C-terminus. This truncated V8 protease, designated V8D, retains its level of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
              Chimeric -
Chimeric -
                                                        Mutant; Staphylococcus truncation; wild type; proteolytic activity; 1
                                                                                                                     Protein encoded by pV8F construct
                                                                                                                                                                                                                 AAW22220 standard; Protein; 537
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus V8 protease mutants - with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-013693/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                         Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 16-17; 42pp;
           Escherichia coli
Staphylococcus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to denaturation
                                                                                                                                                                                                                                                                                                                                                                                                                      532 AA;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96EP-0303939
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125..336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                        ; PCR; polymerase chain reaction; am
fusion protein; beta-galactosidase;
                                                                                       aureus; V8 protease; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "aminoglucoside 3'-phosphotransferase portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "R6 linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "R6 linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8Α
                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protease portion"
                                                                                                                                                                                                                                                                                                                                                                                      Length 532;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                        denaturation;
                                                                        amplification;
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                                                                                                                                                                                                            The invention relates to new mutant Staphylococcus aureus V8 proteases CC which have enzyme activity even under environmental conditions which CC promote protein denaturation. The mutants are based on 3 truncated V8 CC proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino CC acids from the C-terminal of the wild type protease. The mutants also CC contain amino acid substitutions, especially DA4E, N7IS and/or R147K. CC The protein sequence shown here represents a chimaeric protein CC comprising a truncated Staphylococcus aureus V8 protease lacking the CC prepro and C-terminal 53 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the V8 protease fragment is a second R6 linker and a fragment of the C aminoglucoside 3'-phosphotransferase protein. The chimaeric sequence was generated by restriction digestion and ligation from the V8RP7(-) CC sequence (see AAW22218) by using a natural EcoRV site which removed a CC designated V8F, retains its level of activity in the presence of a CC higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                        Query Match
Best Local S
Matches 9
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 19-20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus V8 protease mutants - with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-013693/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohsuye K, Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-1995;
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                                                              289 TGGNSGSPV 297
                                                                                                                        Local Similarity
nes 9; Conserv
                                                                                          1 TGGNSGSPV 9
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                                                                                                                                                                                     537 AA;
                                                                                                                      100.0%; ilarity 100.0%; Conservative 0
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125..339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "E. coli beta-galactosidase"
101..124
_note= "R6 linker sequence"
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10 US-10-008-355-5

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10 US-09-864-761-48349

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13.271 Million cell updates/sec
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Sequence 48257, A	Sequence 43752, A	Sequence 401, App	Sequence 1, Appli	Sequence 444, App	•	Sequence 3, Appli	'n	Sequence 5, Appli	Sequence 224, App	Sequence 13411, A	Sequence 2, Appli	1132	27,	Sequence 5, Appli	•	Sequence 1, Appli	Sequence 1, Appli	Sequence 16, Appl	Sequence 13533, A		Sequence 8, Appli	Sequence 40, Appl	Sequence 34548, A	Sequence 40613, A	Sequence 2, Appli

ALIGNMENTS

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; OTHER INFORMATION: Consensus sequence US-10-008-355-26
                                                                                                                                                                US-10-008-355-25
                                                                                         Sequence 25, Application US/10008355 Patent No. US20020164759A1 GENERAL INFORMATION:
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APPLICANT: Travis, James
APPLICANT: Pottempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 26 LENGTH: 9
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Patent No. US20020164759A1
                          APPLICANT: Travis, James
APPLICANT: Potempa, Jan
APPLICANT: Banbula, Agn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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nes · 9; Conserv
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Banbula, Agnieszka
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; LENGTH: 52
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-008-355-3
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US-10-008-355-3
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Best Local :
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                     SEQ ID NO 4
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APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235,00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
                                                                            CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILLING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
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CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
                                     NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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TYPE: PRT
ORGANISM: Artificial Sequence
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644 TGGNSGSPV 652

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Benbula, Agniesaka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
          8
                                                                                                                 ; TYPE: PRT ; ORGANISM: Porphyromonas gingivalis US-10-008-355-2
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; TYPE: PRT
; ORGANIZM: Porphyromonas gingivalis
US-10-008-355-8
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US-10-008-355-2
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                                              Query Match
Best Local S
Matches S
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APPLICANT: Travis, James
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Matches
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LENGTH: 699
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Matches 9; Conserv
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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APPLICANT: Banbula, Agnisszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
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                                                                                                                                                                     LENGTH: 712
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1 TGGNSGSPV 9
                                              Local Similarity
nes 9; Conserv
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TGGNSGSPV 9
                                              Conservative
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                                                               Score 48; DB 9
Pred. No. 0.86;
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Pred. No. 0.85;
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US-10-008-355-7

Sequence 7, Application US/10008355 Patent No. US20020164759A1

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TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-008-355-7
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Best Local Similarity
"---ches 9; Conserve
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 9 LENGTH: 720
                                                                                          Sequence 6, Application US/10008355
Patent No. US20020164759A1
                                                                           GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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CURRENT FILING DATE: 2001-11-08
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                         APPLICANT:
                                        APPLICANT: Travis, James APPLICANT: Potempa, Jan
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CANT: Potempa, Jan S
CANT: Banbula, Agnieszka
OF INVENTION: Dipeptidylpeptidases and Methods Of Use
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ilarity 100.0%;
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Pred. No. 0.87;
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.87;
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RESULT 11
US-09-864-761-48349
US-09-864-761-48349
Sequence 48349, Application US/09864761
; Patent No. US20020048763A1
; Patent No. US2002004 R
; Patent Application NUMBER: US/09/864,761
; Patent No. US2002004
; Patent Patent Date: 2000-02-04
; Patent Patent Date: 2000-03-05
; Patent Patent Date: 2000-05-26
; Patent Application NUMBER: US 60/207,456
; Patent Patent NUMBER: US 60/207,456
; Patent Patent NUMBER: US 09/632,366
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; Patent Patent NUMBER: US 09/632,366
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; SEQ ID NO 6
; LENGTH: 732
; TYPB: PRT
; ORGANISM: Shewanella putrefaciens
US-10-008-355-6
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; LENGTH: 734
; TYPE: PRT
; ORGANISM: Shewanella putrefaciens
US-10-008-355-5
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CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
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CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER CE CEC 15.000-21-08
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NUMBER OF SEQ ID NOS: 26
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es 8; Conserv
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Banbula, Agnieszka
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Pred. No. 0.89;
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APPLICATION NUMBER: GB 24263.6

NUMBER:

us 60/236,359

2000-09-27 2000-10-

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US-09-815-242-5351
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                                                                                                                                                                                                                                                                                                                            Sequence 5351, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax SEQ ID NO 48349
LENGTH: 74
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Best Local 9
                                                                                                                                                                                                                                                                                                             GENERAL
                APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EST_HUMAN HIT: BE002805.1, EVALUE 8.00e-39
OTHER INFORMATION: SWISSPROT HIT: Q9ZKD2, EVALUE 3.60e+00
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les 6; Conser
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R APPLICATION NUMBER: PCT/US01/00665
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00668
P FTLING DATE: 2001-01-30
P FTLING DATE: 2001-01-30
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APPLICATION NUMBER: 60/206,848
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Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                       Carr, Grant J.
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                                                                                                                                                                         Yamamoto, Robert T
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NITMBER: US 60/234,687
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Pred. No.
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Query Match
Best Local Similarity
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US-09-815-242-12277
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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SEQ ID NO 5351
LENGTH: 240
TYPE: PRT
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                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: F88tSEQ for Windows Version 4.0
SEQ ID NO 12277
LENGTH: 254
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 0111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                      Conservative
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                                                       77.1%; Score 37; 100.0%; Pred. No.
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                                      Mismatches
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19;
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                                                                        OTHER INFORMATION: 1
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION:
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APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                   DATE:
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                               ED IN BRAIN, SIGNAL = 0.98
ED IN BT474, SIGNAL = 1.4
ED IN BONE MARROW, SIGNAL =
ED IN LUNG, SIGNAL = 0.94
ED IN FETAL LIVER, SIGNAL = 1
ED IN PLACENTA, SIGNAL = 2
ED IN HEART, SIGNAL = 1.1
ED IN HELA, SIGNAL = 1.1
ED IN HELA, SIGNAL = 1.1
ED IN HBLLO, SIGNAL = 1.1
                BE939264.1,
                EVALUE 7.00e-04
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PRIOR APPLICATION NUMBER: GB 24263.6
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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CURRENT APPLICATION NUMBER: US/09/864,761
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TYPE: PR
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Gy 1 TGGN8GSPY 9
Db 6 TAGTSGNPV 14

Search completed: December 20, 2002, 12:17:27
Job time: 12.3684 secs
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RESULT 2 G89873 hypothetical protein sspA C; Species: Staphylococcus = C; Date: 10-May-2001 #sequer C; Accession: G89873 R; Kuroda, M.; Ohta, T.; Ucl ma, A.; Mizutani-Ui, Y.; Kc C.; Shiba, T.; Hattori, M. Lancer 377 1727-17240 2011	Query Matc Best Local Matches 1 TG Qy 1 TG Db 233 TG	Comment: lues. Superfam Superfam Superds Superds Superds Superds Superds Superds Superds Superfam Supe	An. J. Bi NTitle: T NETETER: T NACCESSIO NACCESSIO NMOLECULE NRESIDUES NESPETIME NCOMMENT:	N; Title: N N; Referenc N; Accessio N; Molecule N; Residues N; Cross-re N; Experime	RESULT 1 PRSASK glutamyl endopeptidase (EC 3.4.21.19) precursor N; Alternate names: staphylococcal serine protei C; Species: Staphylococcus aureus C; Date: 04-Dec-1986 #sequence_revision 30-Jun-1 C; Accession: A26812; A00966 R; Carmona, C.; Gray, G.L. Nucleic Acids Res. 15, 6757, 1987		33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
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tical protein sspA [imported] ss: Staphylococcus aureus 10-May-2001 #sequence_revisio sion: G89873 n, M.; Ohta, T.; Uchiyama, I.; Mizutani-Ui, Y.; Kobayashi, N Mizutani-Ui, Y.; Kobayashi, N 1255-1240 2001	100.0% larity 100.0% Conservative PV 9 PV 241	may be coccal serine ylococ His, A #statu	4-544, ructur 824; M n n 124;12 strain	uence 812; M L:Y003 strain	(EC 3. hyloco us aur quence 0966 L.		411 451 591 1129 1175 1178 1178 108 108 463 521 531 531 553 783 556 656
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Staphylococcus aureus (strain N315) 10-May-2001 #text_change 22-Oct-2001 aba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K N.; Hayashi, H.; Hiramatsu, K.	ore 48; DB 1; Length 336; ed. No. 1; Mismatches 0; Indels 0; Gaps 0;	to the trypsin-type serine proteinas ase #status experimental <act> ed</act>	l protease. :96922 'T',194-228,'N',230-2	ne protease gene of Staphylococcus aureus, st 3; PMID:3306605 86; PIDN:CAA68434.1; PID:g46687	19) precursor – Staphylococcus aureus serine proteinase sion 30-Jun-1991 #text_change 18-Jun-1999		hypothetical prote magnesium transpor hypothetical prote wall associated pr probable lipoprote probable lipoprote probable membrane probable proteinas hypothetical glyci gene mastermind pr multifunctional am

Lancet 357, 1225-1240, 2001

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R;anonymous, The Xylella fastidiosa COUNTILLIAN CE CONTROLLIAN Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 bel A;Accession: G82627
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrichado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.
                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-716 <SIM>
A;Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSPDB:GN001
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A;Residues: 1-357 <YOS>
A;Cross-references: GB:D00730; NID:g216970; PIDN:BAA00630.1; PID:g216971
C;Superfamily: staphylococcal serine proteinase
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A;Title: Purification, characterization and gene cloning of a novel glutamic acid-speci A;Title: Purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S217
R; Yoshikawa, K.;
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C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
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A; Residues: 1-342 <KUR>
A; Cross-references: GB:BA000018; PID:g13700850;
A; Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ypothetical protein xF1887 [imported] - Xylella fastidiosa (strain 9a5c)
;Species: Xylella fastidiosa
;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-20
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DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2436
                                                                                             A;Cross-references: EMBL:Z12296; NID:g43337; PIDN:CAA78168.1; PID:g43338 C;Superfamily: staphylococcal serine proteinase
                                                                                                                                                                                   submitted to the EMBL Data Library, June A; Description: A gene (sprE) downstream A; Reference number: $25140
                                                                                                                                                                                                                                                  serine proteinase homolog - Enterococcus faecalis C;Species: Enterococcus faecalis C;Date: 20-Feb-195 #sequence_revision 20-Feb-199: C;Accession: $25140
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S25140
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R; Kaneko, T.; Nakamura, Y.;
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A; Gene: alı
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A;Molecule type: DNA
A;Residues: 1-169 <KUR>
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                                                                                                                            A; Molecule type: DNA
A; Residues: 1-284 <SUY>
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DNA Res. 8, 205-213, 2001
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9; Conser
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8; Conserv
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Pred. No. 5.
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Silv
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C;Species: Mus musculus (house mouse)
C;Date: 19-Cct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: A56940
R;Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama, K.
J Biol. Chem. 270, 14471-14476, 1995
A;Title: Strain-specific presence of two TGN38 isoforms and absence of TGN4
A;Reference number: A56940; MUID:95301533; PMID:7540170
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R;Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama,
J. Biol. Chem. 270, 14471-14476, 1995
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C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Nature 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitoch A;Reference number: A71630; MUID:99039499; PMID:9823893

A;Accession: E71729
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C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
                                                                                            A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-363 <KAS>
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A; Residues: 1-315 < AND>
                                                                         A; Residues: 1-363 <KAS>
A; Cross-references: GB:D50031
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                                                                                                                                                                                                                                                                                                      integral membrane protein TGN38B - mouse
                                                                                                                                                                                                                                                                                                                                               RESULT 9
 Best Loc
Matches
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 Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 7; Conserv
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8; Conserv
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87.5%;
               83.3%;
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Pred. No.
                   Score 40;
Pred. No.
   Mismatches
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 PMID:9823893
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hypothetical protein SPBC1685.05 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T39521 C;Accession: T39521 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A. Spanitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; submitted to the EMBL Data Library, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical signaling-associated PDZ domain containing protein [imported] - C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000 C;Accession: T50186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: RC0234
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97729
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                                       A; Reference number: Z21861
A; Accession: T39521
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A; Residues: 1-996 <BAD>
                                                                                                                                                                                                                                  RESULT 12
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A;Gene: SPDB:SPAC23G3.12c
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A; Residues: 1-497 < KUR>
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A; Molecule type: DNA
                 A; Status: preliminary;
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RESULT 13
S63064
                                                                                                    A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: B82414
                                                                                                                                                                                                                                                      C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: B82414
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A;Cross-references: GB:AE004409; GB:AE003853; NID:g9658233; PIDN:AAF96710.1; GSPDB:GN001A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                         A; Molecule type: DNA
A; Residues: 1-476 <HEI>
                                                                                                                                                                   R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February 1996
A; Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces ce
A; Reference number: S67327
A; Accession: S67335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z71399; NID:g1302053; PID:e239802; A;Experimental source: strain S288C R;d'Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YNL123w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein N1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 2
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A;Cross-references: EMB
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A; Residues: 1-997 <DAN>
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A; Residues: 1-997 <DEA>
                                                                                  A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                 leucine aminopeptidase-related protein VCAO812 [imported] - Vibrio cholerae (strain N16
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ce: strain 972h-; cosmid c1685
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77.8%;
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77.8%;
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Pred. No.
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C; Genetics:
A; Gene: VCA0812
A; Map position:
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Search completed: December 20, 2002, 12:11:31 Job time : 25.1579 \ \text{secs}
                                                           밁
                                                                                                                                                                           A; Map position:
A; Introns: 46/1;
                                                                                                                                                                                                       A; Gene: NCSP:B11B22.140
                                                                                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:B11B22.140 A;Experimental source: BAC clone B11B22; strain OR74A
                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-182 <SCH>
                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                        A; Reference number: Z25022
A; Accession: T49812
                                                                                                                                                                                                                                                                                                                                     R;Schulte, U.; Aign, V.; Hoheisel, J.; Brand submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                               C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical
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base, May 2000
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OM protein - protein search, using sw model
                                                                                        GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Run on:

December 20, 2002, 05:38:27; Search time 13.7368 Seconds (without alignments) 27.174 Million cell updates/sec

Title: Perfect score: Sequence: US-10-008-355-26 48 1 TGGNSGSPV 9

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. So	core	Query Match	Length	DB 1	ID	Description
, N	39		418	<u> </u>	ER24_HUMAN	076062
. ω	39	81.2	997	1	YNM3_YEAST	P53920
4	37	•	316	ب	GSEP_BACLI	P80057
υ	37		401	\vdash		P09065
6	36	•	320	↦	CEL1_AGABI	200023
7	36		378	Ļ	ПХВ	Q00205
80	36	•	628	Н	ABFA_ASPNG	O.
9	35	•	108	ب	Y108_NPVOP	**
10	35	•	417	μ	IRX5_HUMAN	_
11	35		521	<u> </u>	YF92_MYCPN	Ψ
12	<u>ω</u>	•	531	_	F88	ω
13	35		584	_	MB3	\sim
14	ဌဌ	٠	1714	щ	SYEP_DROME	O,
15	34	•	303	٢	Y007_MYCLE	032870
16	34	•	325	ب	YF65_STRPN	Q97pn8
17	34		424	۲	CBPT_THEVU	P29068
18	ω 4	•	607	H	V66K_BWYVF	P09506
19	34		843	1	AXN2_HUMAN	Q9y2t1
20	34	•	1035	1	RRPO_BWYVF	P09507
21	34		1286	_	YKV5_YEAST	P28273
22	34		1319	ר	MN1_HUMAN	Q10571
23	34	•	1520	_	ABL_DROME	P00522
24	ω	•	117	Н	WNT6_STRPU	P28097
25	ω	•	221	1	YB31_MYCPN	P75267
26	ω ω	•	261	_	YGCM_ECOLI	P76633
27	33		281	1		200164
28	ω ω	•	282	_	CDX4_MOUSE	007424
29	ω ω		327	_	1	P20009
30	ω ω		328	-		P28294
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ALIGNMENTS

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	entry is copyright. It is produced through a ss Institute of Bioinformatics and the EMBL informatics Institute. There are no restrict fit institutions as long as its content is s statement is not removed. Usage by and f s a license agreement (See http://www.isb-sib to license@isb-sib.ch).	MEDLINE=78212487; PubMed=96922; Drapeau G.R.; The primary structure of staphylococcal protease."; Can. J. Biochem. 56:534-544(1978)!- FUNCTION: PREFERENTIALLY CLEAVES PEPTIDE BONDS ON THE CARBOXYL- TERMINAL SIDE OF ASPARTATE AND GLUTAMATE!- CATALYTIC ACTIVITY: Preferential cleavage: Asp- -Xaa, Glu- -Xaa!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B!- DATABASE: NAME=Worthington-biochem.com/manual; -!- WWW="http://www.worthington-biochem.com/manual/P/STAP.html".	protease."; Infect. Immun. 69:159-169(2001). [3] SEQUENCE OF 69-280. STRAIN=V8;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=20569178; PubMed=11119502; MEDLINE=20569178 PubMed=11119502; Rice K., Peralta R., Bast D., de Azavedo J., McGavin M.J.; "Description of staphylococcus serine protease (ssp) operon in Staphylococcus aureus and nonpolar inactivation of sspA encoded serine	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRALN=V8; MEDLINE-87316953; PubMed=3306605; Carmona C., Gray G.L.; Carmona C., Gray G.L.; "Nucleotide sequence of the serine protease gene of Staphylococcus aureus, strain V8."; Nucleic Acids Res. 15:6757-6757(1987).	1 E

IPR001254; Ser_protease_Try

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[2]
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MEDILINE-98277456; PubMed-9615229;
Lemmens I.H., Kas K., Merregaert J., Van De Ver
"Identification and molecular characterization
gene cluster on human chromosome 11q13.";
Genomics 49:437-442(1998).
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Beccari T.,
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                                                                                                                                                                                        PubMed=11784322;
                                                                                                                                                                                                                                                                                                                                                                                                                             Holmer L., Pezhman A., Worman H.J.;
"The human lamin B receptor/sterol reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                      "Cloning and
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, Della Fazia
nd expression
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Involved in the conversion of lanosterol t ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,
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                                                                                                         YNM3_YEAST STAND
P53920;
01-0CT-1996 (Rel. 34
01-0CT-1996 (Rel. 34
15-JUN-2002 (Rel. 41
Hypothetical 110 9 k
YNL123W OR N1897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF048704; AAC21457.1; A
EMBL; AF023676; AAC21450.1; A
EMBL; AF096303; AAD09765.1; -
EMBL; AF096304; AAD09765.1; -
EMBL; BC009052; AAH09052.1; -
EMBL; BC012857; AAH12857.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01222;
PROSITE; PS0101
PROSITE; PS0101
                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic
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SEQUENCE
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                      SEQUENCE FROM N.A. MEDLINE=97245296; PubMed=9090055;
                                                                       Eukaryota; Fungi; i
Saccharomycetales;
                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sterol biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:11863; TM7SF2
 Pallavicini A.,
            de Antoni A.,
                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                             163 GGNSGNPI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lung, liver, skeletal muscle, kidney, ovary, prostate, but not detected in placenta, spleen, thymus, small int colon (mucosal lining), or peripheral blood leukocytes.

SIMILARITY: BELONGS TO THE ERGA/ERGZ4 FAMILY.

CAUTION: Ref.1 sequence differs from that shown due to sequencing problems as reported in Ref.2.

SMISS-PROT anton.
                                                                                                                                                                                                                                                                   2 GGNSGSPV
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SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603414;
                                                                                                                                                                                                                                                                                          Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; IPR001171; ERG4_ERG24.
01222; ERG4_ERG24; 1.
PS01017; STEROL_REDUCT_1;
PS01018; STEROL_REDUCT_2;
                                                                                                                                                                                                                                                                                                                                    179
418
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13 35
81
102 124
129 148
255 277
285 277
287 304
355 377
299 299
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D'Angelo M., Dal
., Lanfranchi G.,
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                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                  STANDARD;
                                                                                                           Ascomycota; Saccharomycotina; 
; Saccharomycetaceae; Saccharor
                                                                                                                                                                                                                                                                                                                                          46417
                                                                                                                                                                                                                                                                                                     81.2%;
75.0%;
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2; Mismatches
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L -> V (IN REF. 3;
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             Pero
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             'F]
 G.;
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                                                                       Saccharomyces
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            Sartorello
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                                                                                                                    intergenic
                                                                                                                                                                                                                                                                                                                  Length 418;
                                                                                  Saccharomycetes,
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             Pandol fo
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Best Local
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                                                          Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames."; Yeast 13:261-266(1997).
                                                                                                                                                                                                                                           Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E., Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N., "Purification, characterization, cloning, and expression of a
                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl endopeptidase precursor (EC 3.4.21.19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                       Svendsen I.,
                                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                   glutamic acid-specific
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
STRAIN-ATCC 14580;
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis.
Bacteria; Firmicutes; F
                                                                                                                                                                                                                                                                                                                                                                                       endopeptidase)
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                                                                                                                                         "Isolation and amino acid sequence of a
                                                                                                                                                                   MEDLINE=92155199;
                                                                                                                                                                                                                                                                                    MEDLINE=93054737; PubMed=1429718;
                                                                                                                                                                                                                        4580.
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                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B
                                                  SUBCELLULAR LOCATION:
{\tt SWISS\text{-}PROT} entry is copyright. It is produced through a collaboration een the {\tt Swiss} Institute of Bioinformatics and the {\tt EMBL} outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGSSGSPV 240
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S0005067; YNL123W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of cosmid 14-13b from chromosome XIV of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                         Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     997 AA; 1
                                                                                                                                                                                95-316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                    PubMed=1346764;
                                                                                                                                                                                                                                                                                                              AND PARTIAL SEQUENCE
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77.8%;
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                                                                                                    OF PEPTIDES
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                                                                                                                                         glutamic acid
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WITH A STRONG
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SQUETTITION OF THE PROPERTY OF
RESULT 5
HME1_MOUSE
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Best Local
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P09065;

01-NOV-1988 (Rel. (

01-FEB-1994 (Rel. 1

15-JUN-2002 (Rel. 4
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SEQUENCE
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ACT_SITE
    "Expression during embryogenesis of a mouse homology to the Drosophila engrailed gene.", Cell 43:29-37(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0839; VBPROTEASE. SMART; SM00020; Tryp_SPc; 1. PROSITE; PS00672; V8_HIS; 1. PROSITE; PS00673; V8_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as ITS content is in modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                engrailed genes
regions.";
                                                                                                                                                                                                                                                                                                                                                                                          Logan C., Hanks M.C., Noble-Topham S., Provart N.J., Joyner A.L.; "Cloning and sequence comparison of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000126; Ser_proteas_V8.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                              MEDLINE=86079501;
Joyner A.L., Kornl
                                                                                                                                                                   "En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrailed gene: expression during embryogenesis."; Genes Dev. 1:29-38(1987).
                                                                                                                                                                                                                                                         SEQUENCE OF 278-401 FROM N.A. MEDLINE-88112776; PubMed=2892757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Ver.
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Fukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Homeobox protein engrailed-1 (Mo-En-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                      Joyner A.L., Martin G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 GGQSGSPV 265
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                                                                            298-401 FROM N.A.
79501; PubMed=2416459;
, Kornberg T., Coleman
                                                                                                                                                                                                                                                                                                                            13:345-358(1992).
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                                                                                                                                                                                                                                                                                                                                                                        reveal potential
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87.5%;
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POTENTIAL.
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CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
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                                                            sequence
                                                                                                                                                                                                                                                                                                                                                                                               and chicken
                                                                                                                                                                                                                                                                                                                                                                          regulatory
                                                                                G.R.;
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RESULT
CEL1_AG
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PIR; A24778; A24778.

PIR; S13009; S13009.

PIR; A48423; A48423.

HSSP; P02836; 3HDD.
                                                                                                                                                                                                                    _AGABI
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS
       Raguz S., Yaguee E., Wood D.A., Thurs "Isolation and characterization of a
                                             SEQUENCE FROM N.A.
STRAIN-D649;
                                                                               Eukaryota; Fungi; Basidio
Agaricales; Agaricaceae;
NCBI_TaxID=5341;
                                                                                                                  Agaricus bisporus
                                                                                                                                  CELL
                                                                                                                                          Cellulose-growth-specific protein precursor
                                                                                                                                                       01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                01-NOV-1997
                                                                                                                                                                                          CEL1_AGABI
Q00023;
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PROSITE; PS50071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:95389; En1.
InterPro; IPR000747; Engrailed.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L12703; AAA03660.2; EMBL; Y00201; CAA68361.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 321-380 FROM N.A. MEDLINE=91099509; PubMed=1980115; Holland P.W.H., Williams N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                MEDLINE=93012985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservation of engrailed-like homeobox sequences during vertebrate
                                                                                                                                                                                                                                                                    238 SGGNAGSP 245
                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                         1 TGGNSGSP 8
                                                                                                                                                                                                                                                                                                                              ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S Lett. 277:250-252(1990).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE ENGRAILED HOMEOBOX FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                 similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Developmental protein; 52 87 PRO-RICH.
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73
207
312
401
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                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1; HOMEOBOX_2;
3; ENGRAILED; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGRAILED.
                                PubMed=1398098;
                                                                                                      Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                                                                                                                  (Common mushroom)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homeobox; 1.
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371
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75.0%;
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Last annotation update)
                                                                                                                                                                              Created)
                                                                                            Agaricus
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Pred. No.
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POLY-ALA.
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                     Thurston C.F.;
        cellulose-growth-specific gene
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RESULT 7
PLYB_ASPNG
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Best Local S
Matches 6
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DISULFID
CARBOHYD
                                                                                                                                                                                                              PLYB_ASPNG
Q00205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kester H., Hinnen A., Visser J.;
Kester H., Hinnen A., Visser J.;
"Characterization of the Aspergillus regulation of expression.";
Mol. Gen. Genet. 234:113-120(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00734; CBM_1; 1.
Pfam; PF03443; Glyco_hydro_61; 1.
SMART; SM00236; fCBD; 1.
PROSITE; PS00562; CBD_FUNGAL; 1.
                                                                                                                     Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JEC-1998 (Rel. 37, Last annotation update)
Pectin lyase B precursor (EC 4.2.2.10) (PLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M86356; AAA53434.1; -.
HSSP; P00725; 2CBH.
InterPro; IPR000254; CBD_fungal.
InterPro; IPR005103; Glyco_hydro
                                           Kusters-Van Someren M., Flipphi M.,
Kester H., Hinnen A., Visser J.;
                                                                 STRAIN=CBS 120.49 / N400;
MEDLINE=92357005; PubMed=1495474;
                                                                                       SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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or send an email to license@isb-sib.ch).
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use
!- CATALYTIC ACTIVITY: Eliminative cleavage of pectin to give
                                                                                                                                                                                                                                                                              256 SGGNGGSP 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degradation; Hydrolase; Glycosidase;
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30
262
286
292
303
163
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                                                                                                                                                                                                                                                                                                                                                                    AA;
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261
285
320
319
163
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75.0%;
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CELLULOSE-BINDING (
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                   Score 36; DB Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                             Score 36;
                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
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CATALYTIC (POTENTIAL).
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                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                          Mismatches
                                                       de
                                niger pelB
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                                                                                                                                                                  (PLB)
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                                                      Graaff L.,
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                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                            Length 320;
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                                gene:
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                                                       den Broeck H.,
                                 structure
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                *Rlipphi M.J.A., Visser J., van der Veen P., de Graaff L.H.;
*Arabinase gene expression in Aspergillus niger: indications
coordinated regulation.";
Microbiology 140:2673-2682(1994).
-i- FUNCTION: ACTS ONLY ON SMALL LINEAR 1,5-ALPHA-LINKED
-i- FUNCTION: ACTIVITY: Hydrolysis of terminal non-reducing
arabinofuranoside residues in alpha-L-arabinosides.
-i- PARHWAY: INVOLVED IN DEGRADATION OF THE PLANT CELL WALL
-i- PARHWAY: INVOLVED IN DEGRADATION OF THE PLANT CELL WALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
STRAIN=CBS 120.49 /
MEDLINE=95093616; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger.
Eukaryota; Fungi; Ascomycota
Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last a Alpha-L-arabinofuranosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995
01-NOV-1995
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                                         or send an
                                                                 entities
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SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                         SIMILARITY: BELONGS TO FAMILY
                                                                                                                                                                                                                                            POLYSACCHARIDE L-ARABINAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through
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European Bioinformatics Institute. There are no restr
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                                 non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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(Rel. 32, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed-8000538;
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77.8%;
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N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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PECTIN LYASE B.
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                                                                                                                                                                                                                                                                                                                                                                                                                               der Veen P., de Graaff L.H.;
Aspergillus niger: indications
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                                                                                                                                                                                                                       51 OF GLYCOSYL HYDROLASES
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RESULT 9
Y108_NPVOP
RESULT 10

IRX5_HUMAN STANDARD;

ID IRX5_HUMAN STANDARD;

AC P78411; P78416;

AC P78411; P78416;

AC P78411; P78416;
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Matches 6
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 11.7 kDa protein (ORF108).
Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                     Hypothetical SEQUENCE 1
                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                    polyhedrosis virus genome.
Virology 229:381-399(1997)
                                                                                                                                                                                                                                                                                                                  Ahrens C.H.,
Rohrmann G.F
                                                                                                                                                                                                                                                                                                                       MEDLINE=97271300; PubMed=9126251;
MEDLINE=97271300; PubMed=9126251;
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Hydrolase; Gly
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nes 5; Conser
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                                                                      TGGRAGNPI
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75.0%;
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No.
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Lewis M.T., Ross S., Strickland P.A., Snyder C.J., Daniel C.W.;
"Regulated expression patterns of IRX-2, an Iroquois-class home
gene, in the human breast.";
                      SEQUENCE
                                                             Mycoplasma pneumoniae
Bacteria; Firmicutes;
NCBI_TaxID=2104;
                                                                                                                                                     Hypothetical
                                                                                                                                                                          16-OCT-2001
16-OCT-2001
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SMART; SM00548; IRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001356; Homeobox.
InterPro; IPR003893; Iroquois_homeo.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:14361; IRX5.
MIM; 606195; -.
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HSSP; P41778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell Tissue Res. 296:549-554(1999).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE TALE/IRO HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                 MPN592 OR MP250
                                                                                                                                                                                                                       16-OCT-2001
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HOMEOBOX_2; 1.
/ M129
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85.78;
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Last annotation updat
                                                                                                                                                                                                                     Created)
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Last annotation update)
                                                                                 Mollicutes; Mycoplasmataceae; Mycoplasma
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Pred. No. 51;
0; Mismatches
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401F2D865C052AFA
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                                                                                                                                                   precursor (D02_orf521)
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51;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C STRAIN=ACCC 29342 / M129;

C MEDLINE=96177562; PubMed=8604303;

RA Hilbert H., Himmelreich R., Plagens H., Herrmann R.;

RA Frequence analysis of 56 kb from the genome of the bac "Sequence analysis of 56 kb from the genome of the bac Mycoplasma pneumoniae comprising the dnaA region, the cluster of ribosomal protein genes.";

cluster of ribosomal protein genes.";
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YF88_MYCPN
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Q50339;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
Hypothetical lipopu
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MEDLINE-97105885; PubMed-8948633;
MEDLINE-97105885 Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
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Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
"Sequence analysis of 56 kb from the genome of the bacterium
Mycoplasma pneumoniae comprising the dnaA region, the atp operon and
cluster of ribosomal protein genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U43738; AAC43664.1; -. EMBL; AE000025; AAB95898.1; -. InterPro; IPR002414; DUF30/31.
                                                                                                                                                                                    Mycoplasma pneumoniae. Bacteria; Firmicutes;
                                                                                                                                                                                                                  MPN588 OR MP254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae
                                                                                                                                                                      NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Lipoprotein; Membrane; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence analysis of the genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids
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European Bioinformatics Institute.
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Rel. 40, Last annotation update)
Ripoprotein MPN588 precursor (DC
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40, Last sequence 40, Last annotations
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59500
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75.0%;
                                                                                                                                                                                   Mollicutes; Mycoplasmataceae; Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-ACYL DIGLYCERIDE (POTENTIAL)
0E706CDEC8CEEBDA CRC64;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 66.8 kDa protein in TAF40-ERV25
YML013W OR YM9571.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U43738; AAC43668.1; -. EMBL; AE000025; AAB55902.1; -. InterPro: IPR002414; DUF30/31. Pfam; PF01727; DUF33; 1. Pfam; PF01732; DUF31; 1.
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           InterPro; IPR001012; UBX. Pfam; PF00789; UBX; 1. SMART; SM00166; UBX; 1.
                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                       use
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                                                                                                                                                                                                    Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Hypothetical
                                                                  EMBL; Z49810; CAA89939.1; -.
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les 6; Conserv
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                                                                                                                                 ween the Swiss Institute of Bioinformatics and the EMBL outs
buropean Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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protein
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL LIPOPROTEIN MPN588.
N-ACYL DIGLYCERIDE (POTENTIAL).
; 0A3A089261B3C998 CRC64;
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67;
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                                                                                                                    Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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MBL outstation -
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RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Krandell M.D., Zhang Q., Chen L.X.,

RA George R.A., Lewis S.E., Richards J., Zhang Q., Chen L.X.,

RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
                                  A PARTE A PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
SYEP_DROME
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P28668; Q9VCF5;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Bitunctional aminoacy1-tRNA synthetase [Includes: Glutamy1-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase); Proly1-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase); Proly1-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase)].

ARTS-GIJPRO OR CG5394.

Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cerini C., Semeriva M., Gratecos D.;
"Evolution of the aminoacyl-tRNA synthetase family and the
"repolution of the Drosophila glutamyl-prolyl-tRNA synthetase gene.
Intron/exon structure of the gene, control of expression of the two
mRNAs, selective advantage of the multienzyme complex.";
Bur. J. Biochem. 244:176-185(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLLINE=92097547; PubMed=1756734;

Cerini C., Kerjan P., Astier M., Gratecos D., Mirande M., Semeri
Component of the multisynthetase complex is a multifunctional
aminoacyl-trna synthetase.";

EMBO J. 10:4267-4277(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.9%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB Pred. No. 74; 0; Mismatches
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A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Tunner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                      FlyBase; FBGn0005674; Aats-glupro.
Interpro: IPR002106; AARRNA_ligaseII.
Interpro: IPR004046; GST_Cterm.
Interpro: IPR004046; GST_Cterm.
Interpro: IPR004526; GltX_arch.
Interpro: IPR004526; GltX_arch.
Interpro: IPR004454; HGTP_anticodon.
Interpro: IPR004459; proS_fam_I.
Interpro: IPR004499; proS_fam_I.
Interpro: IPR000738; wHEP-TRS.
Interpro: IPR000738; wHEP-TRS.
Interpro: IPR001412; tRNA-synt_Zb.
Interpro: IPR001412; tRNA-synt_Tr.
Interpro: IPR002316; tRNA-synt_pro.
Pfam; PF00043; GST_C; 1.
Pfam; PF00458; wHEP-TRS; 6.
Pfam; PF00587; tRNA-synt_D: 1.
Pfam; PF00749; tRNA-synt_1c; 1.
Pfam; PF00749; tRNA-synt_1c; 1.
Pfam; PF00749; tRNA-synt_1c; 1.
Multifunctional 170 DOWAIN 755 DOWAIN 827 DOWAIN 827 DOWAIN 901 DOWAIN 980 DOWAIN 1055 DOWAIN 1129
                   DOMAIN
DOMAIN
                                                                                                                                                                    PRINTS; PR00987; TRNASYNTHGLU.
PRINTS; PR01046; TRNASYNTHPRO.
TIGRFAMS; TIGR00408; proS.fam_; 1.
TIGRFAMS; TIGR00463; gltx_arch; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
PROSITE; PS50862; WHEP_TRS; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M74104; AAA28594.1; -.
EMBL; U59923; AAC47469.1; -.
EMBL; AE003745; AAF56211.1; -.
PIR; S18644; S18644.
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                                                                                                                                                       Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPRISED OF A BIFUNCTIONAL GLUTAMYL-PROLYL-TRNA SYNTHETASE, THE MONOSPECIFIC ISOLEUCYL, LEUCYL, GLUTAMINYL, METHIONYL, LXSYL, ARGINYL, AND ASPARTYL-TRNA SYNTHETASES AS WELL AS THREE AUXILIARY PROTEINS, P18, P48 AND P43.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

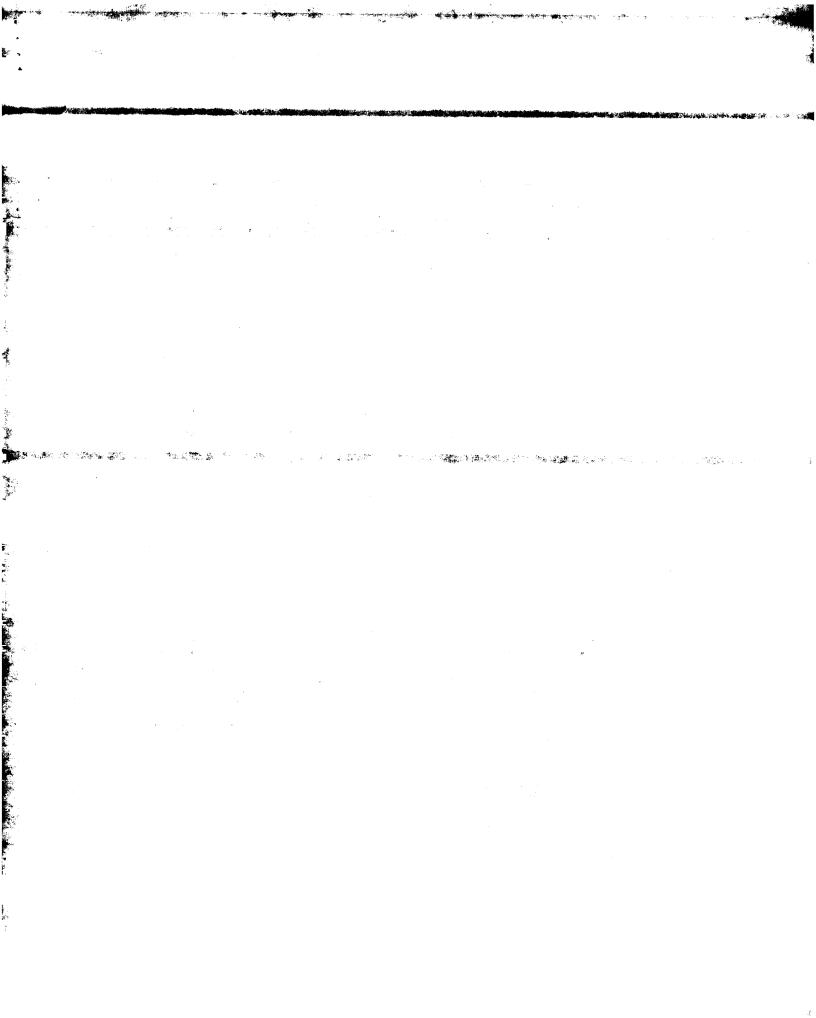
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphosphate + L-glutamyl-trnA(Glu).

CATALYTIC ACTIVITY: ATP + L-proline + trnA(Pro) = AMP + diphosphate + L-prolyl-trnA(Pro).

SUBUNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 6 WHEP-TRS DOMAINS
 enzyme;
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872
946
1025
1100
                                                                                                                                     Repeat
                                                                                                                                                     Protein biosynthesis; Ligase;
 WHEP-TRS
WHEP-TRS
WHEP-TRS
WHEP-TRS
WHEP-TRS
                                                                                                                   GLUTAMYL-TRNA
                                                                                                                   SYNTHETASE
                                                                                                                                                         ATP-binding
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Matches 7
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOO7_MYCLE STANDARD; PRT; 303 AA 032870; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Hypothetical protectin ML0007.
ML0007 OR MLB1770.07.
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                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV0007.
                EMBL; Z70722; CAA94717.1; -
EMBL; AL583917; CAC29515.1;
                                                                                                                                                                                                                                                                                                                                     Squares S., S
Barrell B.G.;
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77.8%;
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ATP (BY SIMILARITY).
TSPLP -> DKSIA (IN REF. 3).
VC -> AF (IN REF. 3).
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I -> S (IN REF. 3).
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Pred. No. 2.4e+02;
1; Mismatches 1;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q-cgn2_1/USPT0_spool/US10008355/runat_17122002_112703_16900/app_query.fasta_1.327
-Q-/cgn2_1/USPT0_spool/US10008355/runat_17122002_112703_16900/app_query.fasta_1.327
-DB-N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_@CGN_1_1_O_@runat_17122002_112703_16900 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=10 -XGAPOP=6 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ID	AAL43635 standard; DNA; 2139 BP.
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AC	AAL43635;
X	<i>,,</i>
DT	05-SEP-2002 (first entry)
XX	
X E	Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence.
XX	Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleavage;
ΧW	DPP-7 inhibitor identification; periodontal disease; gingivitis;
×××	periodontitis.
SO	Porphyromonas gingivalis.
XX	
FΗ	Key Location/Qualifiers
FT	CDS 12139

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Alignment :
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                  The present sequence is that of the N.meningitidis strain BZ163 transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an N-terminal domain, a hinge domain and a C-terminal domain; deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. The positions of the 3 domains in BZ163 are defined by alignment with the IMZ169 sequence. The deletion mutant polypeptid of the invention can generate an immune response against
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                                                                                                                                                      Disclosure;
                                                                                                                                                                                         Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tbp2
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DB; AAR88649.
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                                in BZ163 are derined by deletion mutant polypeptides
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                                                                                                                                                                                                       Human cDNA sequence SEQ ID NO:17412
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                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                    CTCGATCAAAAAATACCACCCGCACGCCTAAGGCATATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGlnAspGlyAlaTrpTyrAsnTyr------HisThrThrGlyLysGly---Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACAAGTTGGACAAAGTATGTTCCTCCAAGGC-----GAGCGCACCGATGAAAAAGAG 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAACAGCAAGTCCGCGATGCAGGCAGGAGAAAGCAGTAGTCAAGCTGATGCTAAAAACG 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scores:
                                                                                                                                                                                                                                                                                                                                                           ProAspLeuGlnArgThrIleSerValAspIleArgTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCCAAGCGAGCAAAACATCGTTTATCGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArg 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGATAAAGAGGGCGGCAACAGGGCGGAATTTACTGTG:
                                                                                                                                                                                                                                                                                                                                                                                       ATTGAGGGCAACGGTTTTTCCGGTACG
                                                                                                                                                                                                                                                                                                                                                                                                            LeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GGGTCTTGGTACGGGCATATTGCCAGCAGCAAGCTGGAGCGGCAATGCT 1746
                                                                                                                                                                               primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2136
 2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                (first
                                                                             2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                      99JP-0248036
99JP-0300253
                                                                                                                                                                              detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTTTGGCGAGAAAAAATTACCGGCACGTTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.732
90.00
37.93%
21.84%
8.97%
                                                                                                                                                                                                                                                                                    cDNA;
                                                                                                                                                                                                                                entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474
                                                                                                                                                                                                                                                                                    2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;
                                                                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 G; 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
                                                                                                                                                                                                                                                                                                                                                                                       -GCAAAAACTGCTGAATTAGGTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
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밁
                                                  Вb
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                                                                                                  Db
                                                                                                                          Qy
                                                                                                                                                     В
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                                                                                                                                                                                                       Вb
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                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                        US-10-008-355-2_COPY_522_712 (1-191) x AAH17774 (1-2794)
                                                                                                                                                                                                                                                                                                                                              Best Local S
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                             Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 560; full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 17412; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for full-length cDNAs defined in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-318749/34.
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 745
                         111
                                                  709
                                                                                                   589
                                                                                                                                                     634 GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC
                                                                                                                                                                                                       574
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                                                                                                                                                                              53
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                                                                                                                           72
                       GlnLeuHisIleAlaPheLeuSerAsnAspIleThrGly-----
                                                               GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                       GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                                                                                                                                                                                                              GlyArgAlaLeuProSerAspAla----AsnPheThrMetArgMet--
                                                                                                                                                                                                                                                       AGCTATGGGGTCAGAAGGGGCCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC
                                                                                                                                                                                                                                                                              AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                                                                                           ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
                                                                                                                                                                                                                                                                                                                                                            Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
, Sugiyama
                                                                                                                                                                           SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tion describes primer sets for synthesising 5602 defined in the specification. Where a primer se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INST
                                                                                                                                                                                                                                                                                                                                  1.22
89.50
38.32%
25.15%
8.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                       687 A;
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T, Wakamatsu

    AGCCGGTTTGAAAACTACGGAGACAAGTTTGCAGAG

                                                                                                                                                                                                                                                                                                                                                                                                                                       851
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- AACGATGTGATTGGCTGCTTTGCGGATTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       735
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ı A, Nagai K
                                                                                                                                                                                                                                                                                                                                                                                    Length: Matches:
                                                                                                                                                                                                                                                                                                                                                           Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                  ----AAGTCCACCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       521
                                                                                                                                                                                                                                                                                                                                                                                                                                       Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K, Y, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                2794
42
22
56
47
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e detection
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777

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RESULT 4

RAALSOLT 4

AALSOLT A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                    of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                       immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI59418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI59418 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-)
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                                                                                                                                                                                                gene therapy. A composition containing a polypeptide or polynucleotide
                                                                                                                                                                                                                                           invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
  thrombolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AN AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-442253/47.
DB; AAM40262.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCGCAGTGGAGTTCAACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C
Wang Z
Zhou
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
; 2000US-0662191.
; 2000US-0693036.
; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ı C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0488725.
2000US-0552317.
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"Ashrman T, Xu
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                                                                                                                                                                                                                                                                                                                          10078pp; English.
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cancer diagnosis and therapy, drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nen R, Ma Y,
Ku C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ب</u>
screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
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RESULT 5
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                                07-FEB-2001.
                                                      EP1074617-A2
                                                                                                                         Human cDNA sequence SEQ ID NO:14778
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to the comprises a 1'-end sequence and an oligonucleotide comprising a sequence complementary to a complementary to an oligonucleotide comprises a 3'-end sequence, where the coligonucleotide which comprises a 1'-end sequence, where the coligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and compressed therapy and the specification. The primers are useful for synthesising polynucleotides, are full-length cDNAs. The primers are also useful for the compression of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH3316 to AAH3362 and CC AAH3363 to AAH318742 represent human cDNA sequences; AAB9246 to AAH35893 represent human amino acid sequences; and AAH31629 to AAH3362 conference inventions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises: (a) an oligo-dT primer and an oligonucleotide complementary
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                                                      GGCACTGGGAAG----
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                                                                                                                          GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC-----TATGGCTATGGA 1047
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                                                                                    ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, for responsible for
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                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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2000US-0649167.
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                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                 Human
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AAI61204 standard;
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                                Homo sapiens
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                                                                                                                                                                                 polynucleotide SEQ ID
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                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                           Alignment
                                                                                                                                                                                                                                                                                                                                                                     the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity such as: Inmune system suppression, Activin/inhibin activity, Chemotactic/Chemokinetic activity haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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19-JUL-2000;
03-AUG-2000;
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25-APR-2000;
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DB; AAM42048.
ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
                                GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC
                                                                               GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                                                                                      GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet-----
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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           RESULT 8
and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase and in recombinant production of (II). The polymerase mapping, and in recombinant production of (II). The polymerase mapping and in recombinant production of (II).
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23-AUG-2000;
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Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from W.
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                                                                                                                                                                             AAV34396;
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            EP877086-A2
                                        Synthetic.
                                                     Flavivirus
                                                                                pathogen;
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                                                                                                                       Yellow fever infectious cDNA clone YFiv5.2/DD
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SerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                         ATTGTTAACAGGAACGGAGAGGTGATTGGGCTGTACGGCAATGGC-----ATCCTT
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Query Match:

Best Local Percent Similarity:

Similarity:

7.76 89.50 39.22% 25.49% 8.92%

Length:
Matches:
Conservative: Mismatches: Indels:

10892 39 21 46 47 8

Alignment

NO . .

US-10-008-355-2_COPY_522_712 (1-191) x AAF83821 (1-10892)

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                            prM-E protein deleted, truncated or mutated so that functional yellow fever virus prM-E protein is not expressed and also integrated into the genome of the yellow fever virus a nucleotide sequence encoding a prM-E protein of a second, different flavivirus so that the prM-E protein of the second flavivirus is expressed. The chimeric live, infectious, attenuated virus is used to prepare medicaments for preventing or treating flavivirus infection in a patient. The yellow fever virus vector produces its gene product (tumor antigen or cytokine) in cells of the lymphoid or reticuloendothelial system or in a precursor of these systems in patients with cancer. Flaviviruses replicate in the cytoplasm of cells so that the virus replication does not involve integration of the viral genome into the host cell. The present sequence represents a chimeric DNA derived from yelllow fever virus and Japanese encephalitis virus.
                                                                                                                                                                                                                                                             The invention relates to a chimeric live, infectious, attenuated virus comprising a yellow fever virus with the nucleotide sequence encoding
                                                                                                                                                                                                                                                                                                                                                  Chimeric live, infectious, attenuated yellow fever viruses used for preventing and treating diseases caused by flaviviruses have prM.E nucleotide sequence from a second, different flavivirus as function yellow fever prM-E is not expressed.
 Sequence 10892
                                                                                                                                                                                                                                                                                                                Disclosure; Page 200-215;
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chambers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flavivirus febricis.
Japanese encephalitis virus
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RESULT 11
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the
                                                                                                        Claim 1; SEQ ID 1; 2504pp; French
                                                                                                                                                                                                                                                         11-APR-2000;
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                                                                                                                                   New nucleotide sequence useful in lactis and related species -
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Arabidopsis thaliana; thale cress; plant; transgenic; GMO; stress; metabolic pathway; biosynthetic pathway; nutrition;
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Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                 Arabidopsis thaliana
                                                                                21-AUG-2002
                                                                                                                                          ABQ65948 standard;
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86.00
36.71%
21.74%
8.57%
                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                           -----PheAspGlyAsnTrpGluAlaMetSerGlyAsp
                                                                                entry)
                                                polynucleotide SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                        PheAspLysAsnGlyArgLeuIleGlyLeuAla-----
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                   GMO; disease;
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fungicide;

91

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Pred. No.:
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                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                          US-10-008-355-2_COPY_522_712
                                                                                                                                                                                                                                                                                                                                                                                                                       Gorlach J, , Rameaka JG,
                                                                                                                                                                                                              The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ6542-ABQ66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides,
                                                                                                                                                                                                                                                                                                                                                                                                     Garcia CA,
Hurban P;
                                                                                                                                                                                  insecticides and antibiotics).
Note: The sequence data for this patent did not form
specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                      New nucleic acid that hybridizes to Puseful e.g. for preparing transgenic or altered metabolism -
                                                                                                                                                     Sequence 651 BP; 185 A; 110
                                                                                                                                                                                                                                                                                                                   Claim 1;
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(LEDF/)
(WOES/)
(HAAS/)
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(PAGE/)
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(YUYY/)
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5
             AspAlaAsnPhcThrMetArgMetSerTyrGlySerIleLysGlyTyrGluPro---Gln
GATGCTAAGGGAACAAGATTTAGCAAGGAAAGGGAAAATTGTGGGTCTTGATCCAGATAAT 131
                                                                                                                                Scores:
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LEDFORD B L.
WOESSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
ALLEN K.
HOFFMAN N.
HURBAN P.
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PAGE A.
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RAINES T M.
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                                                                                                                                                                        e sequence data for this patent did not form part of the printed ation, but was obtained in electronic format directly from the seqdata.uspto.gov/sequence.html?DocID=999909770149.
                                                                                                                                                                                                                                                                                                                  SEQ ID NO 525;
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Kricker N
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A, Mathew AV,
er M, Slater T,
                                                               0.521
85.50
38.16%
27.63%
8.52%
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pavis KR, /
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Matches:
Conservative:
Mismatches:
Indels:
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Allen K,
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Hoffman
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RESULT 13
AAC46293
ID AAC46
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
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25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
16-APR-1999
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21-APR-1999
21-APR-1999
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          06-MAY-1999;
06-MAY-1999;
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09-MAR-1999
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         99US-0125788.
99US-0126785.
99US-0127462.
99US-0128734.
99US-0128734.
99US-0130077.
99US-0130047.
99US-013048.
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28-OCT-1999
28-OCT-1999
17-MAY-2001
                                                             Staphylococcus epidermidis vaccination; endocarditis;
                                                                                                                   03-SEP-2001
                                                                                                                                                             AAH53441 standard;
                    WO200134809-A2
                                        Staphylococcus
                                                                                            S. epidermidis
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                                                                                                                                                                                                      ATTGACACAGTTGTCCGAACAGTTCCGTACCTCATT
                                                                                                                                                                                                                          Valasp-----IleargTyrValLeuPheMetIle 175
                                                                                                                                                                                                                                                                                         GGGCCATTGCTTGATTCTTATGGCCATACCATAGGTGTGAACACTGCCACATTCACCCGA
                                                                                                                                                                                                                                                                                                                                                        GlyGln---LeuHisIleAlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSerGly
                                                                                                                                                                                                                                                                                                                                                                              GATCTAGCTGTGTTGAAGATTGAAACTGAGGGACGTGAACTAAATCCTGTTGTTCTCGGT
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                                                                                                                                                                                                                                                                     AsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIleSer
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                                                                                                                                                                                                                                                                                                                                    GGGAAGAGTATTTCAGAAGCTATACAAACCGATGCTGATATTAACTCAGGCAATTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCCAATGATCTACGCGTAGGTCAAAGTTGCTTTTGCGATTGGGAATCCATATGGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             ValLeuGluLysGlnAspProLysSerAspGluPheAlaVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspAlaAsnPheThrMetArgMetSerTyrGlySerTleLysGlyTyrGluPro---Gln
                                                                                                                   (first
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99US-0161359.
99US-0161361.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0162142.
                                       epidermidis
                                                                                           open reading frame nucleotide sequence SEQ ID
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99US-0161405
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99US-0160989
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the sepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of s. epidermidis infections, e.g. endocarditis. AAH33971 to AAH55090 represent specifically claimed s. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4456 to 4472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH52304 to AAH53970 represent nucleic acids (I) encoding (II), given in AAG81454 to AAG83120, from Staphylococcus (I) and (II) can have antibacterial activity and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding
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P-PSDB; AAG82591.
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AAAAAAGAATCT----GTTGAGGATACTGCTAAAGTTTTAGGCAGAATGTTTGATGGA
                                                                     GCATCTATTGATCTAGGTGCACACCCTGAATTTTTAGGGAAAAATGATATTCAATTAGGA
                                                                                                                                         AAGAATATTGCTTTACTCTTCGAAAAGACATCTACTCGGACGCGTGCCGCATTTACAGTT 231
                                                                                                                                                                           GlyGlnLeu------
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                                                                                                                                                                                                                                                                                 TTGCTAAAAGAGTATGATCTTACAGGTGAAGAATTT------GAAGGTCTAATCGAT
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                                 AsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGly
                                                                                                                                                                                                                                               LeuPheArgThr---LysAsnTyr------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are present for SEQ ID NO:4455 to 4464.
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                             CC (bleb) preparation from a Gram-negative bacterium for use as a vaccine.

CC The blebs of the invention are improved with respect to their communogenicity and toxicity by the introduction of one or more genetic changes to the chromosome of the bacterium from which the blebs are compassed in the downregulation of immunodominant non-protective antigen compasses in the downregulation of immunodominant non-protective antigen compasses modified Gram-negative bacterial strains from which the bleb compasses modified Gram-negative bacterial strains from which the bleb compasses modified Gram-negative bacterial strains from which the bleb compasses modified or negative bacterial strains from which the bleb compasses modified or negative bacterial strains), comparations are made, a vector suitable for performing recombination compasses considered nucleic acid sequences used in such a vector, and an immunoprotective and non-toxic Gram-negative bleb phost, or killed whole coll vaccine suitable for paediatric use. The bleb preparation is useful in the manufacture of a medicament for immunising a human host against a company of the compasse caused by infection of one or more of the following: Neisseria compania. The invention are asequinosa, Chlamydia trachomatis, and chlamydia trachomatic, and chlamydia trachomatic of the infunction are used in the performance of homologous recombination events up to the provide sequences of the concease or decrease expression of that gene. Immunoprotective and conceased to the provide sequence of the conceased to the provide whole cell vaccines are more of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine; genetically modified; protective antigen expression; LPS detoxification; LPS; lipid A; homologous recombination vector; immunisation; immunoprotective; non-toxic; paediatric; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 46; Page 81; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide useful for outer membrane vesicle preparation from Gram-negative bacterial strain for vaccination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-138654/14
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Poolman J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to a genetically-engineered outer membrane vesicle
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Db 427			Db 328	Оу 118	Db 295	Qу 98	Db 256	Оу 78	Db 205	Оу 62	Db 175	Qy 42	Db 121	Qy 22	Db 61	Qy 2	us-10-008	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:
PROMESTICAL ACCUMENTATION																	008-355-2_COPY_522_712 (1-191) x AAF91391 (1-731)	Alignment Scores: 1.24 Score: 83.00 Percent Similarity: 35.068 Best Local Similarity: 21.268 Query Match: 8.288 DB: 22
ASPILEATGTYTVAI 1/1 ::: CCTAAGGCATATATC 468	GCGAAAACTGCTGACTCAGGTTTTGAT	LeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGlu:::	ACCGCTGACAACAGGCAGGCGGCAACCTTTACCATTGTGGGCGAT	SerAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArg	AATTTCGGTACGAAAAAATTAACGGCACGTTA	AlaGluAsnGlyGlnLeuHisIleAlaPheLeu	TCCGATAAAGAGGGCGGCAACAGGGCGGACTTTACTGTG	GluPheAlaValGlnGluAsnIleLeuAspLeu		HisThrThrGlyLysGlyVal	CGG	LeuDroSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGlu 61	GAACAAGTTGGACAAAGTATGTTCCTCCAAGGCGAGCGCACCGATGAAAAAGAG 174	AlaGlyLeuArgGluMetTyrProGlyArgAla	AAAAACAGCAAGTCCGCGATGCAGGCAGGAGAAAGCAGTAGTCAAGCTGATGCTAAAACG	IleGlnAlaAspAlaMetAlaAsnAlaTyrAla	x AAF91391 (1-731)	Length: 731 Matches: 37 Conservative: 24 Mismatches: 71 Indels: 42 Gaps: 6
	426	157	372	137	327	117	294	97	255	77	204	61	174	41	120	21		

Search completed: December 21, 2002, 02:00:26 Job time: 749 secs

Sequence 731 BP;

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-O=Cegn2_1/USPTO_spool/US10008355/runat_17122002_112704_16920/app_query.fasta_1.327
-O=Cegn2_1/USPTO_spool/US10008355/runat_17122002_112704_16920/app_query.fasta_1.327
-DEGENEND1 -OFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL-0 -LOOPEXT=0
-UNITS-blts -START=1 =END=-1 -MATRIX=blosum62 -TRANS=hunan40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_CGCN_1_1_1616_erunat_17122002_112704_16920 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1960.027 Million cell updates/sec
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_othee:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_wrt:*
80: em_sy:*
39: em_htg_othem:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	0 00)		Ω	c c cc; Res
443	36 37 40 40	3 3 3 3 3 3 5 5 6 7 8 8 9 8 9 8 9 8 9 8 9 8 9 9 9 9 9 9 9	17 18 19 20 21 22 23	7 9 10 11 12 13 14	Result NO. 1
885.5 84.55	86.55 86.55		8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	91.5 90.5 90.5 90.8 90.8 89.5 89.5 89.5	Score 334 176.5 175 101.5 93 91.5
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3750	315079 315079 3832 7756 10760 9293	10862 10862 10862 10862 10862 10862	3158 3513 3514 10862 10862 10862 10862 10862	180688 187710 1554 2143 2163 2794 2908 2956 3048	Length 10689 10689 253217 10811 10811 204050 11581 79718
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AY091427 AF114386 AY056227 AF050190	DE040653 MPULM03 CAJFLAAB AF202168 AF204612 AF01022 AF016285	AFU52446 FLYF17DG YFU17066 YFU17067 YFU21055 YFU21056 YFU21056 YFU54798 YFU54798	BC002564 HSA7509 AK022863 AR124177 AR002387 AF052437 AF052438 AF052439 AF052444	CNS01RG9 CNS01DVI A1U52600 A47465 AWTBP2163 AK023006 BC021506 BC021713 BC009988 BC0277844	ID AE004008 AC016590 AE011732 AE007581 AFA12H2
AY094427 Arabidops AF114386 Arabidops AF056227 Arabidops AF056120 Campyloba	10 20 13	40000000	Homo sap Homo sap Homo sap Sequence Sequence Sequence Yellow 8 Yellow 9 Yellow 4 Yellow 4 Yellow	Humar Humar Avian Avian equenc Homo 6 Mus Homo Homo Homo	Description AE004008 Xylella f AC016590 Homo sapi AE011732 Xanthomon AL646073 Ralstonia AE007581 Clostridi AL807577 Aspergill

ALIGNMENTS

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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
2036571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The genome sequence of the plant pathogen Xylella Xylella fastidiosa Consortium of the Organization Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
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Xylella fastidiosa 9a5c,

AE004008 AE003849

AE004008.1 GI:9106961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submission
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                                                                                                                                                                 complement(119. .367)
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                                                                                                                                                                                                                                                                                                                                                                 organism="Xylella fastidiosa 9a5c"
                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brazil
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                                                                                                 complement(2918. .3202)
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//note="hypothetical protein; identified by sequence
rimilarity: nutative; ORF located using Glimmer/RBSfinder"
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1351. .1662
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similarity; putative; ORF located using
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Glimmer/RBSfinder"
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                        LeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAsn 47
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similarity; putative; ORF located using
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similarity; putative; ORF located using Glimmer/RBSfinder"
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/gene="XF1878"
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AYIAGGFRGVKNV"
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DQQPSSGGASSPPSSSGTAWPSFCSWASVVCDFIDWVKSDEFLKKPLVPPDVPYVDKL
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SSVISDGVSTSATFEARSTALVNGVRYYTVPVDISASTLGSLAKVAVRRGMAFYNVYS
MLSGLINGAGWVIDELTHEVMSGPALKEIPVGTVAWWWQRPGDGHVFYSVTPQGLIAP
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/gene="XF1877"
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located using Glimmer/RBSfinder*
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PHIVMCFLVAWGFHFLFTVVRD"
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/protein_id="AAF84683.1"
/db_xref="GI:9106968"
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/protein_id="AAF84685.1"
/db_xref="GI:9106970"
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/protein_id="AAF84682.1"
/db_xref="GI:9106967"
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/protein_id="AAF84684.1"
/db_xref="GI:9106969"
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similarity; putative; ORF located using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACTCCGGATCGCCAGTCTTAGATGCCCCACGGAAAATTGGTGGGTTTAGCATTTGACGGT
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Consensus quality: 207648 bases at least Q40 consensus quality: 225569 bases at least Q30 consensus quality: 225569 bases at least Q30 estimated insert size: 250510; agarose-fp estimation Estimated insert size: 249417; sum-of-contigs estimation Quality coverage: 9.03 in Q20 bases; agarose-fp estimation Quality coverage: 9.07 in Q20 bases; sum-of-contigs estimation.*
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                         Submitted (04-DEC-1999) Production Sequencing Facility, Do Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 90 On Apr 20, 2001 this sequence version replaced gi:7711568
                                                                                                                                                                                          Project Information
Center Project Name: 940643, BC905667
Center clone name: CITB-E1_3220F14
                                                                                                                                                                                                                                                                                     Center: Joint Genome Institute Center Code: JGI
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DOE Joint Genome Institute.
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SEQUENCE, 39 unordered I
AC016590
AC016590.6 GI:13699590
                                                                                                                                                       Summary Statistics
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CTD-3220F14, WORKING DRAFT
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others

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consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCAAGCCGTCTATCCTGACGCCAACAGCACCCTGCGCGTGACCTTCGGCCGCGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLys 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scores:
                                                                                                                                                                                                                                                                           CTACAACAAGGCCGAACACCCGTTCGATCCAGGTCGACCTGCGCTACATGCTGTGGAACA 4304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uPheArgThrLysAsnTyrGlyArgTyrAlaGluAsn-----GlyGlnLeuHisIleAl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCGTGACCATTGCGCCGACGGCACCACCTGGACCGCGTTCACCACCGTCAATGGCGTG
                                                        the complete genome. AE011732 AE008923 AE011732.1 GI:21107
   Xanthomonas
                                                                                                            AE011732
Xanthomonas axonopodis
Xanthomonas axonopodis
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170641
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164353
164453
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144950
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185147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CalTech human BAC library D" 62867 c 62532 g 61752 t 3820 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .253217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CTD-3220F14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144949: contig of 4236 bp in length
145049: gap of unknown length
164352: contig of 19303 bp in length
164452: gap of unknown length
170540: contig of 6088 bp in length
170640: gap of unknown length
185046: contig of 14406 bp in length
185146: gap of unknown length
222209: contig of 37063 bp in length
222209: contig of 30908 bp in length
253217: contig of 30908 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.94e-07
176.50
54.19%
30.32%
17.60%
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pv. citri str.
pv. citri str.
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                                                                                                            0811 bp DN
by. citri str.
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Matches:
Conservative:
Mismatches:
Indels:
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4604

4664

DNA 306,

linear

section

BCT 110

29-MAY-2002 of 469 of

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FEATURES
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitajima, J.P.
Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
Nature 417 (6887), 459-463 (2002)
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Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xanthomonas.
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                                                     complement(1840.
/gene="fecA"
                                                                                                                                                                                                                                                                                                                                                         /product="threonine 3-dehydrogenase"
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/translation="MKALVKERANKGIWPTPGPNevliklegypvp"/
/translation="MKALVKERANKGIWP"/
/translation="MKALVKERANKGIWP"/
/tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(293. .1315)
/gene="tdh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="pathovar: citri"
complement(293. .1315)
                                                                                                                                                                                             FKGLTVQGIYGRKMYETWYKMTQLVLSGFPLHKVLTHQLPIDDFQKGFDLMEEGKAGK
                                                                                                                                                                                                                                                   SLKDVMADLHMEGFDVGLEMSGNSRAFNDMLDCMYHGGKIAMLGIMPRGAGCDWDKII
                                                                                                                                                                                                                                                                                          DVIGEDVLITGAGPIGIIAAGICKHIGARNVVVTDVNDFRLKLAADMGATRVVNVSKT
                                                                                                                                                                                                                                                                                                                                      RPHLCPNTVGIGVNVNGAFAEYMVMPASNLWPIPDQIPSELAAFFDPYGNAAHCALEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="identified by sequence similarity; putative;
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="XAC1022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xanthomonas axonopodis pv. citri str. 306"
/strain="306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:190486"
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                                                                                                                                                                                                                                                                                                                                                                                                     /y1. .7054
/gene="XAC1026"
6791. .705/
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SQNTCAPLIKSLDHSWKAGHGQDPARWAEYDAWVPYKGELTMGYFQRHDIPYYHALAD
AFTICDGYYCSLHGPTNPNRWLFTGTSGPSVGNVGAQAVTADDGNWTADMARDKPG
YAALQWTTYAQRLQAAGVDWRVYQEYDNFGCNSLAYFSHYRDLRTDDERYLRARACVP
GSTAGNAATTQAEHLVAAIAADVRANRLPQVSWVIPPTAYCEHPEAPPAYGESLVARL
IDALFANPEYWAKTALIINYDENDGFFDYYAPLARADRAWGRSUVDTHGEVYDGVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGTRVPMLVISPWTRGGWVNSQVFDHTSVLRLLERRFGVAEPNISPWRRAVSGDLTS
VFDFRKPDDSALSALPSVDDYRARTAAVRDKPLPSAPAAATMPRQEPGQRPARALPYA
LQVHARVQEGAAVQLQFVNSGAAAAAFNVYNSAAGGGPWYYTVLPGTQLDDAPIGATH
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QWGDGNRLSLEVDTSRRKEYDYMDLSLTSQRALGWUYDYLQPDWAATAVQWARAYQNTG
ATSGVANGYPQSLAGLESDYSWLDASYYAGGGLRRDNLAGLSGTFYFGGATLDASGY
HGNRGEGQWVTPYVRTSAQIPVSMRTTDYGLDRFGGTSALKWSWGNHDLEVGAWAENA
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QDIEQLTPGSSAFKAVEKLPGVQFQSADPFGTYEWSTQVTLHGFDQSRLGYTLDGIPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMSLDVKF"
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VVATSGKDVVGIPALMFSSSASYQIGNLRLDLDGKYVDKRYITFLNDSQVPSYWLFNA
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LNYGAKALSTTTRAQSLVPTTALAQGRIRAEDNFLPQLGINYKLDERQDLYASYSKNI
                                                                                                                                                                                                                                                                                                                                                                        6791. .7054
/gene="XAC1026"
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/gene="XAC1025"
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/gene="XAC1024"
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translation="MGAVVALGGCTASFVSPQGLVVTNHHCAYGAIQLNSTAQKNLIK/
                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                 /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
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located using Blastx/Glimmer/Genemark"
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/protein_id="AAM35906.1"
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located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                        transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MRPNLFAVSVLATLAVAASAQAGEGMWVPQQLPEIAGPPQQAGL"
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                                                          185
                                                                                                                                                                                                                                              145 GlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIle 164
                                                                                                                                                                                                                                                                                                                                           125 GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAsp 144
                                                                                                                                                                                                  TTGAAGGAACTC 7224
                                                       IleGlnGluLeu 188
                                                                                                       GCCGTGGACGGCCGCTATCTGCGTTGGATCATGACCGAGGTCGCTCCGGCGCCCACAGCTG
                                                                                                                                                     SerValAspIleArgTyrValLeuPheMetIleAspLysTrpGlyGlnCysProArgLeu 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mrillarhgetpwnaegryqgqidiplspvgegqaralgerlhs
LQIDRAVASPLSRAQATAKAALGASRQALLQTDADLQEIAHGEWEGLLASEINDKDPA
RLRAWREEPDTVLMPGGESLRQVLDRSWRGLMRAADGLGAHDTLLVVAHDAVNRVILC
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/codon_start=1
/transl_table=11
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7051. .7236
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/gene="folc"
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located using Blastx/Glimmer/Genemark; dihydrofolate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="phosphoglycerate mutase"
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/db_xref="GI:21107168"
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/transl_table=11
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/protein_id="AAM35910.1"
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REFERENCE
AUTHORS
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AUTHORS
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KEYWORDS
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Pondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex Christian.Bucher@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., Chandelr,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,M., Schiex,T., Siguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia solanacearum.
Ralstonia solanacearum
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 204050)
Boucher, C.A.
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2 (bases 1
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AL646073.1 GI:17429991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://sequence.toulouse.inra.fr/R.solanacearum.html.
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TFETREGILKHCSRNNAATLGDLGRRRLEGQQPSLEAQCLANLADEVAYNHDIDDGLRL
SGLITTLEQLEGVPLWARHRREAEAAFPGVGGRRMINETIRRIINALIVDLIAGTRAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene name confidence : probable predicted by Codon_usage predicted by Honology predicted by FrameD"
complement(1298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="small molecule metabolism; central intermediary metabolism; nucleotide hydrolysis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(115.
/gene="dgt"
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/gene="dgt"
                                                                              complement(1298.
                                                                                                                                                                                                                                                                                                                          /product="PROBABLE DEOXYGUANOSINE TRIPHOSPHATE TRIPHOSPHOHYDROLASE PROTEIN"
                              /note="RSc2969;
                                                                                                     LFRVFLEDPRLLPPQYQARDPADQPRWIAHYIAGMTDRYAIKEHRRIFAVEVL'
                                                                                                                            TGAAPQSIDDVRAAPPLVAFSEPMRDEARVLKRFLFDNLYRHYLVMRMAAKARRIIED
                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="RSc2968; RS01329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ralstonia solanacearum"
/strain="GMI1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Product confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /EC_number="3.1.5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:305"
                                                                                                                                                                                                                                                                                                                                                                                                                            'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Qualifiers
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                         RS01328"
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                                                                              2404)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable
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'translation="MITVDUDIGERAYPIHIGTGLLSQAELFAPHIRGTRAVIVTNET VAPLYAARVEAAIRSLGKTVDMVVLPDGESFKTWETLNKIFDALLASGADRKTTLVAL GGGVIGDMTGFAAASYKRGVPF1QVPTTLLSQVDSSVGSKTGLNHPLGKNMIGAFIQ QAVLADIDTLRTLPPRELAAGMAEVIKHGAIADADYFAWIERHIAGLNACDADLMAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3114. .5258)
/gene="pilQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVPVIFEHEGEMGFRDRETQMIDELTARHGVVVATGGGAVLRPENRAFLRERGTVIYL RANPHDLYLRTRHDKNRPLLQTENPRARLEELHAIRDPLYREVAHFVIETGKPTVAQL VNMVLMQLEVAGIVVPPAASSPTSQVSRQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted by Codon_usage predicted by Homology predicted by FrameD"
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Gene name confidence : probable
                             RLNYQRADDVRNMLLGTGGTAGGGAAASRILSKRGSLTSDARTNQLFVSDIPSKLEEV
QAFLLKIDIPVRQVMIEARIVEADDTFSRNLGAKLGFAAKTNGAGYGNTYSNVVSPVT
                                                                                                                    FAAPAPTAGVERPSVRNIDFRRGEELAGRVVVDLSTSNSAINIAQQGQNLVVDFAGAT
LPQSLRRRFDVSDFGTPVQAMRATDNGTGARLVIEPRGNWQYSSYQTDTQFVVEVRPT
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PASNAVERVEQASTATRVVLDLARQSQYKSEIRGNQYVLTLGAAPTASATPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted by Codon_usage predicted by Homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="structural elements; cell exterior; surface
structures"
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/gene="pilQ"
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/note="Product confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKLGQAFVTTVPDTDLRATLQHAVLRPPTEAPVA"
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/db_xref="GI:17429993"
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predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="PROBABLE SHIKIMATE KINASE I PROTEIN"
/protein_id="CAD16679.1"
/db_xref="GI:17429994"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by Homology predicted by FrameD"
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KDATWDNSAAVSLPANGINGVNAASVAVSLFNAGAGRFLALELSALEADGRGKIISSP
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                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/transl_table=11
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Gene name confidence : pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="aroK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=1
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/function="small molecule metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                          /product="PROBABLE FIMBRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE-4 ASSEMBLY SIGNAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable
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Db 190879 ATCACCAACTGCCACGTGCTGCGCGGCGGCAAGCAGGTCTGGCTCAAG---
                                                                                                                                                            US-10-008-355-2_COPY_522_712 (1-191) x AL646073 (1-204050)
                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                  Alignment
                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                16
{\tt MetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluunder} \\
                                                                                                                                                                                                                                                                                                                                                  Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Product confidence :
Gene name confidence : prob
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Product confidence : probable gene name confidence : probable predicted by Codon_usage predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAD16682.1"
/db_xref="01:17429997"
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elqlpnrtemdalladvnhagiargltfdlfrogsavvkpyyaeipvsvkvngryhdm
alfaadvaalsrivtlrnialtgnkdgsmvmearaeavraldpdeqaaqrkaaavvkg
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/gene="pil0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGTAEWKEKMTTLKVQEGAQ" complement(5797. .6462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="RSc2972; RS01325"
complement(5255. .5800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNLFKSTAKTNDRTELLVFLTPRVLSDQLSLK"
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NKDSLGTQTTNGFAINTKHVQTQVLVENGGTVVIGGIYTQNERTDVNKVPLLGDIPVL
                                                                                                                                                                                                                                                                                                                                                                                                                        structures"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPLEAFKLLGTMKRNGESEAVLSVGDKTQHVHVGQYIGQNYGRIVRIGDQELTLRELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKGQVMTRRQVTRLIHLSPLCLAVVLAACGASADDELEQWMQQA
RSTVSTRLAPLPEPKPYAPREYTTTKQTDPFSVQKVAELSRAQNESPEPGHRREPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="PROBABLE FIMBRIAL TYPE-4 ASSEMBLY LIPOPROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structures"
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                                                                                                                                                                                                                                                                                                                                                                                              /note="Product confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="RSc2974; RS01323"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="pilN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="PROBABLE FIMBRIAL TYPE-4 ASSEMBLY MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                           'function="structural elements;
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101.50
41.61%
24.09%
10.12%
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                                                                                                                                                                                                         Gaps:
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Indels:
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probable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q., Gibson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I., Tatusov,R.L., Sabathe,F., Doucette-Stamm,L., Soucaille,P., Daly,M.J., Bennett,G.N., Koonin,F.V. and Smith,D.R. Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum
J. Bacteriol. 183 (16), 4823-4838 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-JUL-2001) GTC Sequencing Center Production, Finishing, and Bioinformatics teams, Genome Therapeutics
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Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                          /gene="CAC0653"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="ATCC:824"
                                                                                                                                          \primetranslation="MHLLIVEDDEELSILLKKGLKQYNCTCDISHDGEDGLYNLEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity:
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                                         68 TyrAsnTyrHisThr------
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                                                                                          TTTGTATATGAGAAAAAAGGTGGAGTAATTGATGTATATAAAACGGAAAAAGGAAGATAT 1157
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9575.
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IKNYILDLFTDKSFGIVEFYSKVFLHNLKLNVLEFKSQSEFVERLEFI IDSINKIQAK
GINENDFVKYKRIFYKDLKSYHKEYKYYQSEE IIKECINNFLYDEELMTLSNEYEACN
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/protein_id="AAK78638.1"
/db_xref="GI:15023536"
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9167. | 9370
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lmegglþngtahftehlcidsnvaylknygkyvednnilggytmeggtvyyfbotton
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kdkfplýkikciekmefgsvksfhdkwykponsaicicgdiansdienkiskyfsefk
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7765 . 9084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAIVGLNGCGKTTLIKLLTRLYDPTEGEIYIDNINIKEFNIESLYKGIGIVFQDFMKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Hypothetical protein, CF-26 family"
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/translation="viii"
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/protein_id="AAK78636.1"
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KDCSRCWAARLCNVCYSHCYTDGKLDMKEKKRYCIRSRERALRSLVFYHKCAEINPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CAC0660"
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Aspergillus fumigatus.
Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 79718)
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Woodward,J.R., Denning,I
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/db_xref="taxon:5085"
/db_xref="taxon:5085"
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/gene="AfA12H2.01"
/join(2. .1327,1382. .4864)
/gene="AfA12H2.01"
/note="Similar to Saccharomyces cerevisiae hypothetical
/note="Similar to Saccharomyces cerevisiae hypothetica
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                                                                                                 /translation="IESHGLFFLCSQSRRVRAFAITVLRLITEFDRALGKENTRIIRV
LEADAHBILNVWDEQLSVAERSRIQKGRRKSASHNTLIELCSSEVSYDSTLWSKVFPN
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MTAEILLEQWKLYLVMACTTLNSVGAQSQSQLAHARKSSKGSQQSQDKISSARSL
FAFVIPLLSAERSSIRNAIVMALGSINKNLYRTFLESLQYAVTTCNEEAKIRIGAHHR
SPSSPRRNRKTDRLRTEVTHYYKLTSHFLREPEVYNDDWIVNNLVTYTKDLRIFLSDA
EVQNDWEFQRLRFHYCGLMEELFEGINRTKDPSHWIPFESRKSAFSLMEDWCGYSPNQ
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                                                                                                                                                                                                                                                                                 /product="conserved hypothetical
/protein_id="CAD37139.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Aspergillus
/strain="Af293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denning, D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knowles,D.G., Hall,N.,
D.W., Anderson,M.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GluPheGluProAspLeuGlnArgThrIleSer
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CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fumigatus"
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                                                                                                                                                                                                                                                                                                                                                        protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wellcome Trust Genome
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Barrell, B
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APVILLIEAVVKLIHVUILIAMITVQEQAREMIVHIIHELIAKKIDDDAPAATRQ
GIEDFVESIRRSDPKVWEYEDNUDKEDGDGGRVPLSMSTVTRQVVNFTSFAYEGVS
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QREDSVGVYSPNTLMPQVSGHTLRPTTHARSVTSPANNLYPPSSSNVQFSTPPLGFSE
SAYLSDDEFEDGLYEFDGRLTMNKPPTVFHNSQGRSVTDGSSSLESMIRSGMRRLTGG /gene="AfA12H2.03"
/note="Similar to Schizosaccharomyces pombe hypothetical
/note="Similar to Schizosaccharomyces pombe hypothetical
62.9 kDa protein c29a10.02 in chromosome ii spbc29a10.02
or spbc365.18 TR:094381 (EMBL:AL034463) (567 aa) fasta
scores: E(): 3.1e-05, 33.85% id in 319 aa
pfam:PF00076;RNA recognition mottif. (a.k.a. RRM, RBD, or
RNP domain);0.16;codon 51-119 SYRSNDISRYQLMKNPASNMPESSWSTRNSPATWETTPVYHGRLYGRHAIPNNASASS SKTVMPSTPCVKARSQGSSPQKENMDVDCLSPISPCKEALMTSPRSAL" complement(join(11060...11087,11156...11243,11312...12053, QLISLPDSKSRNSRLKDLEDKTSTNIYCTNVPITWTEADLRHHFEPYHVVSEKISRDE KTGVSKEVGFARFDTREIAEKVLGEFHNISKNGVKLLLRFADTKAQKMLKQQSNERRA YRAGEYNYSVEVVQGSTPSPSLQRLQQTANHLSPNSQVSYPSPVGVGSTWTPATSISP /product="conserved hypothetical protein"
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/REGITNVYIRGFLPOTTDEMLHSYAARFGKLDRCKAYVDLDTGLCKGYVKAASSMSAC prosite pattern:PS50102; Eukaryotic RNA Recognition Motif (RRM) profile;;10.326; codon 126-203" 10253. .10567)
/gene="AfA12H2.03"
join(9141. .9470,9608. STGRCWPMEVNNPVPGVVETAPASRGYEGGFGVGLMKKDLRLAITAAKESGTPLALAE
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join(9141...9470,9608...9697,9745...9839,9901...10219, GTMKVEVAQSAREVAEQSTVMITSLPEPEHVKDVFHSILKHGDLPALEEERLFIDTST IDPASSKEIANAIHSTRTGHFVDAPMSGGVVGARAGTLSFMFGASSQSGGLIERVRAV LMLMGKKAWHLGPPGAGVSGKLANNYILAINNIATAEAMNLGTRWGLDPKSLADMINT /product="putative 3-hydroxyisobutyrate dehydrogenase" /protein_d="CAD37140.1" /db_xref="Gi:21527808" /translation="MSLTPTVSLRIRGFSVPKSLLSSLSSVPQLQRSQARTFSTTLQR signature Confirmed by InterPro eMOTIF pattern match.;8e-5;codon 50-63" QVVPKNMVQERKDITPAPPDVKSLPYVADLGTVLPVGNKQAGLSLGQVALIFLVDLMV GPDSQRNMVAAILPWVQTMELQIDPNGGETAKSYMLLANLFEITIRCGNILPNEVQAL DATWGFIGLGOMGYLMAKNLRAKIPATDTLLVRDVNENATTRFVEETKEAAKSSGAAD prosite profile:PS00895;3-hydroxyisobutyrate dehydrogenase WQALATGPHGGNVQLVLDFIISLCLERKEQNFVEYAKQVVVFLSGTPAGSKVIEFFLM EERQQKSSRLQDFDISISDKTTAVYKLAQFETSRRLAKQHSDLAFTLFSEFSLHFRNV VSERPKALESYFEVVTQVLIEHTDYPLGFWRILGAVLVTLGNQKREIRMKSAKLLRIL complement (join (11060. /gene="AfA12H2.04c" /codon_start=1 ESGSVLQFDVGRMLSWIDIIFNTLSDKWHAIGRRALKNLIIHNKEHSYLLERAIEMCH /gene="AfA12H2.04c" /codon_start=1 .10567 .9697,9745. .9839,9901. .10219, .11087,11156. .11243,11312. .12053

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domain;3.6e-27;codon 305-388 prosite profile:PS00039;DEAD-box subfamily ATP-dependent helicases signature Confirmed by InterPro eMOTIF pattern match;8e-5;codon 198-206"
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                                                                                                                                                                                                                                                     GHLPKERQTILFSATQTKKVSDLARLSLQDPEYVAVHETASSATPSKLQOHYVJTPLP
QKLDILMSF IRSNLKSKTMVFLSSGKQVRFV KSFRHLOPGI PUMHLHGRQKQGGRLD
IVTRFSQSKHQVLFSTDVAARGLDFAVDMVIQLDCPEDADTY IHRVGRTARVEREGR
AVLFLDPSEEEGMLKRLEQKKVPIEKINIKANKQQSIKDQLQNMCFKDPELKYLGQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Similar to Schizosaccharomyces pombe probable ATP-dependent RNA helicase spac1093.05 TR:Q9UTP9 (EMBL:AL132839) (735 aa) fasta scores: E(): 1.5e-118.53.67% id in 749 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Similar to Schizosaccharomyces pombe DNA j domain containing protein spbcl734.05C TR:074746 (EMBL:ALO31856) (209 aa) fasta scores: EC): 2.1e-17. 41.62% id in 185 aa prosite pattern:PS50076;dnaJ domain profile.;11.351;codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTSDTHPNPKLRVEHSADPGOGVADGTOSQHYRPAYELTEDQEERLGRILNNPFSISQ
SSSLTSFYHSFAPQTPDVGRCSNATELD"
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SLNVIATALSRYKLSELSLSYMGKDCLVLLILFLASLHPHPPDEEGGLAYIRAI
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TDPHGANLTHFDPTDSGWPDFMRIHPVIDWHYAEIWAFIRHLGLKYCSLYDRGYTSLG
                                                                                                                                         FISYVKSVYIQKDKEIFKLKELKLDEFAASLGLPGAPRIKFIKGDDTKORKNAPRAAA
HLLSDDDDTDEEDGEKKSKKKEEPQVRTKYDRMFERRNODVLAEHYSKLINDDGTMDL
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                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MAPAAGPRTGKHAKPQRSKTLKRKRGQEELSSLIQRVEDLDLKG
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/protein_id="CAD37144.1"
/db_xref="GI:21627812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(13982. .15673,15761. .15826,15869. .16207,16235. .16311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical DNA j domain containing protein"
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/db_xref="GI:21627811"
/translation="MSSDEQDALDALEKEASDFIKVCFSIRCVSIILFLYAVLDLQPG
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/gene="AfA12H2.05c"
                                      LESLATGLLG"
                                                                        EEEETLVQLPPYEGDQDDEAPRPSKKPKVKFTEANDREEAEPCDQAAHTPRQIQTLED
                                                                                                               EEQFKARGDAKDQQAKFLAEEAERTRLADMEDKEIAKQKRREKKEKRKARERELLAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam:PF00271;Helicase conserved C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             smart:SM00487;DEAD-like helicases superfamily, catalytic
domain;5.6e-53;codon 66-269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain; 8.5e-25; codon 305-388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smart:SM00490; helicase superfamily c-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16336. .16414)
/gene="AfA12H2.06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPESDIKLQYRKKSLLIHPDKTKNPAAPDAFDRLKKAQTTLLDEKARAYLDECIADAR
RLLIREHKYTVDSPELQTEEFKKEWRQKTVQVLLEEEARRRRQLKAKLQEEGREKRKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(12955. .13492,13553. .13589,13671.
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/protein_id="CAD37142.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="AfA12H2.06"
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.17294,17367. .17626,17679.
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.17880,17933. .17974,
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                                                                                                                                                                                                                                                                                                                    CNS01RG9/c
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                               REFERENCE
                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                    KEYWORDS
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                                                                                                        ORGANISM
     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspLeuGlnArgThrIleSerValAspIleArgTyrValLeuPheMet------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCGGTCTGCGGCGGCGGATGTGGTGGAAGAATATCAAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluPro 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGACAGAGAATATTGAGCGGGTACTGGAGCGTGGTGAGCGAATTGATTTGTTGGTCGAT 75153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---CCTTCGAGCACTGATTTCTCTCTCTCCCTGCATACGGCTGCGCCGCTTTCAACTCG 75306
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                                                                                                                                                                                                                                  CNS01RG9 14 DNA sequence BAC R-638I2 of library RPCI-1 from chromosome 14 DNA sequence BAC R-638I2 of library RPCI-1 from chromosome 14 of Homo sapiens (Human), complete sequence at.173871
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 180688)
                                                                                                              Homo sapiens
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     Heilig, R.,
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/gene="AfA1212.07"
join(17274. 17294,17367. 17626,17679. 17880,17933. 17974,
18033. 18181,18245. 18709,18759. 19248)
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Petit, J.L., Vico, V.,
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[2 of library RPCI-11
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  Wincker, P.,
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Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artigu
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,
Gyapay,G., Saurin,W. and Weissenbach,J.
Sequencing of the human chromosome 14
segref@genoscope
                                   National de Sequencage
                                                                                                                                                                                                                                                                                                                Artiguenave, F.,
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- Web : www.genoscope.cns.fr)
On Jun 27, 2001 this sequence version replaced gi:11611154 Assembly program: Phrap; version 2.0 Quality coverage: 6.78x in Q20 bases; sum-of-contigs Downstream BAC (overlapping the SP6 end) : R-362L22 (AC=AL135838) The following BAC sequence is oriented from the T7 to the Upstream BAC (overlapping the T7 end): R-775615 Web site: http://www.genoscope.cns.fr/ Contact: SeqRef@genoscope.cns.fr Submitted (26-JUN-2001) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail : Center: Genoscope / Centre National de Sequencage

/organism="Homo sapiens" /db_xref="taxon:9606" Location/Qualifiers of bases with a quality value ¥ 40 •• 99

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Identified using t
86726. .86933
/note="matching EN
RHdb:RH68412
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1 (bases 1 to 187710)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14

    Web: www.genoscope.cns.fr)
    On Oct 5, 2001 this sequence version replaced gi:13872725
    ----- Genome Center

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                                                                                                                                                                                                                                                        Assembly program: Phrap; version 2.0 Quality coverage: 6.92x in Q20 bases; sum-of-contigs
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope
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                                                                                        Avian infectious bronchitis virus s
Avian infectious bronchitis virus
Viruses; SSRNA positive-strand virus
Coronaviridae; Coronavirus.
1 (bases 1 to 1554)
Sapats, S.I., Ashcon, F., Wright, P.J.
Novel variation in the N protein of
                                                                                                                                                                                                                                                                                                                                                                            PheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArg
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2 (bases 1 to 1554)
Sapats,S.I., Ashton,F.,
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 AATGGAAGT
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On Feb 28, 1997 this sequence
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Direct Submission
Submitted (14-JAN-1997) Sandra I.
Submitted CTRO. Crn Flemington Rd
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Sapats, S.I., Ashton, F., Wright, P.J. and Ignjatovic, J.
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EPKPRSRSASKDRKSAPATPKQQRAKKVQKKEEEERSHSEDEKEVNNQLEYDDDVSDI
PNKIDWGEGAFDDINI"
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GDLEWGDPNDDVVWYKAKGADTSKIGNYGVPDPDKPEDQAPLFE LEGGPNNFRWDFIAL
SRGRNGSSSLATSRESSRFGSRDSSRCRQRSKYDEIGLIDRAAKIINQQQKUGARISKO
KANEMAERKYHKRAVAPGKRIDEVFGQRKKGKAPNFGDDKMIEEGVKDGRLTAMLNLV
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/protein_id="AAB48161.1"
/db_xref="GI:1515373"
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ProGlnAspGlyAlaTrpTyrAsnTyr-----
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Millet, M.B., Lissolo, L., Mazarin, V.,
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RQQSVLDKVKTDDGSNLYTSPYLTQSNHQNGSTNSGAKQPKREVKDYKNFKYVYSGWF
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SENSKLTTVLDAVELKLGDKEVQKLDDRSNAAQLVVDGIMIPLLPETSSSGNNQANQG
SKSKLTTVLDAVELKLGDKEVQKLDDRSNAAQLVVDGIMIPLLPETSSSGNNQANQG
TNGGTFATTKKPDHTPESDKKDAQAGTGYNAGATASMTAGTTNGKTETTDGKELGG
SWYGHIASTSTSASGNASDKEGGNRAEFTVNFGEKKITGTLTAENRQBAFTTIDGKIEG
SWYGHIASSTSASGNASDKEGGNRAEFTVNFGKKITGTLTAENRQBAFTTIDGKIEG
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/translation="MNNPLVNQAAMVLPVFLLSACLGGGGSFDLDSVDTEAPRPAPKY
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1 (bases 1 to 2163)
Legrain, M., Findeli, A.,
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/protein_id="CAA90598.1"
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/strain="BZ163"
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                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAACAGCAAGTCCGCGATGCAGGCAGGAGAAAGCAGTAGTCAAGCTGATGCTAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAla
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                                                                                                                                                                                                                                                                                                                                                                           ProAspLeuGlnArgThrIleSerValAspIleArgTyrVal 171
                                                                                                                                                                                                                                                                                                                                                                                                                ATTGAGGGCAACGGTTTTTCCGGTACG-----GCAAAAACTGCTGAATTAGGTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlnAspGlyAlaTrpTyrAsnTyr-----HisThrThrGlyLysGly---Val 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTCCAAGCGAGCAAAACATCGTTTATCGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGlu
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yanamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
                                                                                                                                                    AK023006.1 GI:10434722
oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2
clone_lib:NT2RP2 clone:NT2RP2005168.
                                                                    Isogai,T.,
                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                            to Homo
                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                            AK023006
                                                                                                        Mammalia;
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                       3006 2794 bp mRNA linear sapiens cDNA FLJ12944 fis, clone NT2RP2005168, como sapiens mRNA for EIB-55kDa-associated prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTCTTGGTACGGGCATATTGCCAGCAGCACAAGCTGGAGCGGCAATGCT
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61. .2133
/gene="tbp2"
/product="transferrin-binding
480 c 529 g 448 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -AATTTTGGCGAGAAAAAAATTACCGGCACGTTA---
                                                                                                        Eutheria; Primates; Catarrhini;
                                                                    Ota,T.,
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90.00
37.93%
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    ACCGCTGAAAACAGGCAGGGAGGCAACCTTTACCATTGATGGTAAG

                                                                   Hayashi, K.,
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Conservative:
Mismatches:
Indels:
                                                                   Sugiyama, T.,
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38
28
66
42
                                                                                                      Hominidae;
                                                                                                                                                                         cDNA to
                                                                 Otsuki,T.,
                                                                                                                                                                                                                                         05168, highly protein.
                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                         PRI 01-AUG-2002
highly similar
                                                                                                        Homo.
                 Yamamoto, J.,
                                                                    Suzuki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1746
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JOURNAL
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164 IleSerValAspIleArgTyr 170
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                                                                                                                                                                                                                                                                                                                                                                                    685
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                                                                                                                                                                                                                                                      111 GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly--------
                                                                                                                                                                                                                                                                                                                                          92
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                                                                                                                                                                                                                                                                                                                                GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                        ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
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                                               CGAATCCAGAAGGAAGCCTTGGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT 897
                                                                                                                             TGTGGAAATGACGTGGAACTGTCTTTTACCAAGAATGGAAAGTGGATGGGCATTGCTTTC
                                                                                                                                                     ---GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                                                                                                                                 GGCACTGGGAAG------AAGTCCACCAAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC-----TATGGCTATGGA 684
                                                                                      AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                                               -----AACGATGTGATTGGCTGCTTTGCGGATTTTGAA 777
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Isogai, T. and Otsuki, T.
Direct Submission
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mailigenomics@fhri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'-& 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEDO human cDNA sequencing Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor cells after 2-weeks retinoic acid (RA) induction."
851 c 735 g 521 t
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/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 55 Row: i Column: 3
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcGnhgrl.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Bastrian,S.D.,McCloskey,J.C.,
Maduro,Q.L., Massello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC021506 2908 bp mRNA linear ROMUS musculus, Similar to EIB-55kDa-associated protein MGC:36621 IMAGE:5347099, mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the following selection criteria: GenomeScan gene
EPDPHVVRIGWSLDSCSTQLGEEPFSYGYGGYGKKSTMSRFENYGDKFAENDVIGCFA
DEECGNDVELSTTKNGKWMGIAFRIQKEALGGQALYPVLVKKGAVEFNFGQRAEPYC
SVLPGFTFIQHLPLSERIRGTIGPKSKAECEILMWGLPAAGKTTWAIKHAASNPSKK
YNILGTNAIMDKMRVMGLRRQRNYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQT
NVYGSAQRRKMRPFEGFQRKAIVICPTDEDLKDRTVKRTDEEGKDVPDHAVLEMKANF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="MGC:36621 IMAGE:5347099"
/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
                                                                                                                                                                 ERELEADDDPGLPGHNNEEVETEGGSELEGTAQPPPPGLQPHPEPGGYSGPDGHYVMD
NITRONGYESTPVIKQENESSYDRRPLDMEPQQOVYHPELKTEMKQEAPPSFLPPEAS
QLKTDREPGFONKKRPPEENRGRYSFEHREDRRGRSPQPPAEEDEEDDFDDTVAALDTV
CDLHFKVARDRSSGYPLTIEGFAYLMSGARASYGVRRGRVCFEMKINEEISVKHLPST
                                                                                                                                                                                                                                                                                                    /product="Similar to E1B-55kDa-associated protein 5"
/protein_id="AAH21506.1"
/db_xref="G1:18204832"
/translation="MDVRRLKVNELREELQRRGLDTRGLKAELAERLLAALEAEEPED
                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Mam6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                              TGTGCTGGGAATTTAACTTT 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGAAATGATGTGGAGCTTTCTTTTACCAAGAATGGCAAGTGGATGGGCATTGCCTTC
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Submitted (08-AFR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                              BC027713 2956 bp mRNA linear PH Homo sapiens, Similar to ElB-55kDa-associated protein MGC:16645 IMAGE:4123077, mRNA, complete cds.
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Direct Submission
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GlyArgAlaLeuProSerAspAla----AsnPheThrMetArgMet--
                                                                                                         AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                                                                                                                                                                                                                                          Similarity:
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 722
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NNRGSYNRAPQQQPPPQQPPPPQPPPPQPPPPSYSPARNPPGASTYNKNSNIPGSSA
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/protein_id="AAH27713.1"
/db_xreff="GI:20379474"
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/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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                                                                                                                                                                     Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y. Wetherby K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-t., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                       Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 26 Row: h Column: 8. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Submitted (02-JUL-2001) National Institutes of
Gene Collection (MGC), Cancer Genomics Office,
Institute, 31 Center Drive, Room 11A03, Bethesd
                                                                                                                                                              Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                              111 GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly-----
                                                                                                                                                                                                                                                  925
                                                                                                                                                                                                                                                                                                                                                                        850
                                                                                                                                                                                                                                                                                                                                                                                                                                    790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                             901 GGCACTGGGAAG-----
                                                                                                                                                                                                                                                                               92
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TGCGCAGTGGAGTTCAACTTC
                                                                                                                      TGTGGAAATGACGTGGAACTGTCTTTTACCAAGAATGGAAAGTGGATGGGCATTGCTTTC 1053
                                                                                                                                      ---GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                  GluAsnTleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                  ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
                                                                                                                                                                                                                                                                                                                                                                     GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC-----TATGGCTATGGA
                           IleSerValAspIleArgTyr 170
                                                         CGAATCCAGAAGGAAGCCTTGGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT 1113
                                                                                        AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyArgAlaLeuProSerAspAla----AsnPheThrMetArgMet----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scores:
                                                                                                                                                                                                                                                                                                                                                                                                  SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mdvrrlkvnelreelQrrgldtrglkaelaerlQaaleaeepdderelDaddepgrpghineempwtilpgrtnstipkssnkktsQatrgdhwkwsssrpi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MGC:16706 IMAGE:4127873"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="PH108-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Unknown (protein for MGC:16706)"
/protein_id="AAH09988.1"
/db_xref="GI:14603013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=]
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38.32%
25.15%
8.92%
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                                                                                                                                                                                                                                                -AGCCGGTTTGAAAACTACGGAGACAAGTTTGCAGAG-----
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1134
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Matches:
Conservative:
Mismatches:
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22
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vordent:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassifit
15: sp_bacteriap::
16: sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             December 20, 2002, 07:26:30 ; Search time 48.3158 Seconds (without alignments) 38.381 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                    sp_invertebrate:*
sp_mammal:*
sp_mhc:*
 sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                   sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                              671580
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	6	ហ	4	u	2	. —	Result No.
38	39	39	39	39	40	40	40	40	41	42	43	48	48	48	48	Score
79.2	81.2	81.2	81.2	81.2	83.3	83.3	83.3	83.3	85.4	87.5	89.6	100.0	100.0	100.0	100.0	Query
253	997	996	499	396	497	363	353	315	284	169	217	716	357	342	316	Match Length DB
N	ω	ω	10	12	16	•	11	16	N	16	N	16	N	16	Ν	
P96151	074325	Q9P7S1	Q9LK70	Q8VA04	Q92J35	Q62314	Q62313	Q9ZDX8	Q47809	Q8YM87	Q9AJX0	Q9PC94	Q04186	Q99V45	Q9FBG1	ID
P96151 vibrio chol	074325 schizosacch	Q9p7s1 schizosacch	Q91k70 arabidopsis	Q8va04 apple stem	Q92j35 rickettsia	Q62314 mus musculu	Q62313 mus musculu	Q9zdx8 rickettsia	Q47809 enterococcu	Q8ym87 anabaena sp	Q9ajxO staphylococ	Q9pc94 xylella fas	Q04186 staphylococ	Q99v45 staphylococ	Q9fbg1 staphylococ	Description

443 543	40 41 42	39 39	3 3 3 3 6 5 4	332	30 31	27 28 29	25	23 24	18 19 20 21	17
37 37 37	37 37	37 37	37 37	37	37	37 37	37	ມພູພູພູ		ير ھ
77.1 77.1 77.1		77.1 77.1 77.1			77.1 77.1		77.1 77.1		79.2 79.2 79.2	
1377 1844 1971	1117 1254 1306	817 857 1008	449 461 590	284 370	240	233 239 5	235 235	627 1097	394 398 476	289
404	4	16 5	16 16	16 16	16	16 16		10	112	7
Q9UPN5 Q22579 Q9NTT5	Q9H5J5 Q9NSL4 053775	Q93560 Q8T070 Q98KC9	083887 Q9Y414 Q8Y3Y8	Q93JK9 Q9KZV9	Q9KH50 Q53781	Q99T60 Q9KH49 Q53782	Q9KH51 Q9FD08	Q9D2L9 Q9SRP2 Q8RY22	Q8QR15 Q8VE75 Q8VLD4 Q9FYL4	CORMOR
homo sapien caenorhabdi homo sapien	Q9h5j5 homo sapien Q9nsl4 homo sapien O53775 mycobacteri	9 പ്			S	Q99t60 staphylococ Q9kh49 staphylococ O53782 staphylococ	נט נט	Q9d219 mus musculu Q9srp2 arabidopsis Q8ry22 arabidopsis		Dogmos rhizohium 1

ALIGNMENTS

Query Matc Best Local Matches	SQ SE						DR In				RT St								OC Ba						AC 09	P.H.G	RESULT
Query Match Best Local Similarity 100 Matches 9; Conservative	Hydrolase; Serine I SEQUENCE 316 AA;	500673;	t; PS50240;	SMART; SM00020; Tryp_SPc;	PRINTS; PR00839; V8PROTEASE.	Pfam; PF00089; trypsin;	Interpro: IPRO01254;	MEROPS; S01.269;	EMBL; AJ293885; CAC06168.1;	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases	Staphylococcus warneri M. ";	"Characterization of the gene encoding glutamyl endopeptidase	Kodaira K.I.;	SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	3I_TaxID=1292;	Staphylococcus.	Bacteria; Firmicutes: Bacillus/Clostridium group:)M.	Glutamyl endopeptidase	01-MAR-2002 (TrEMBLrel.	_	01-MAR-2001 (TrEMBLrel.	O9FBG1;	I OGENCI DEFITM	
.0%; Sc .0%; Pr	Serine protease. 316 AA; 34296 MW; 4E	V8_SER; 1.	TRYPSIN_DOM; 1.	ур_SРc; 1.	8PROTEASE.	psin; 1.	4; ser_protease_rry.		C06168.1;	to the EMBL/	neri M.";	of the gene enc			0) to the EMBL/				es; Bacillus/Cl		dase.	20, Last	16, Last	<pre>Lrel. 16, Created)</pre>	IMPART, FAT,		
Score 48; DB 2; Pred. No. 1.3; Mismatches 0;	4E997A5A111DDB40						V8 V8	1		'GenBank/DDBJ d	,	oding glutamyl			GenBank/DDBJ d.				ostridium grou			annotation update)	sequence update)	.ed)	O DA	7	
Length 316; ; Indels 0;	CRC64;									atabases.	,	endopeptidase			atabases.				p: Bacillales:			ate)	e)				
; Gaps 0;												of															

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"Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
                                                                                                                                                                                                                                                                              Q04186 PRELIMINARY; PRT; 357 AA. Q04186; Q04186; 01. Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NAR-2002 (TrEMBLrel. 20, Last annotation update) Glutamic acid specific protease prepropeptide (EC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99V45
Q99V45;
Q1-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PROOB39; VBPROTEASE.
SMART; SMO0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsumoto
                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001254; Ser_protease_T: InterPro; IPR000126; Ser_proteas_V8 Pfam; PF00089; trypsin; 1. PRINTS; PR00839; V8PROTEASE.
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Cui L., Oguchi A., Aoki K.-I., Nagai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315); MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                             Yoshikawa
                                                                                                                                                  NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233
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       7.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease; 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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           Shin M.,
                                     Tsuzuki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Serine protease; Complete proteome 36977 MW; 5AEF42DCE01C4B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                         Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (strain Mu50 / ATCC 700699), and (strain N315).
Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00.0%;
       H., Fujiwara
Yoshida N.,
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       T., Nakamura Teraoka H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRYPSIN FAMILY.
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                                         (H)
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                                                                                                                                                                                                                         Bacillales
                                                                                                                                                                                                                                                                                                     3.4.21.19).
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                                         Iwamoto
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Ito T.,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Hypothetical protein Xf1887.
                                                                                                                                                                                                                                                                                                                                                                                                         Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PC94;
Q9PC94;
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InterPro; IPR00126; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
                                  "The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AE004008; AAF84693.1; -.
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EMBL; D00730; BAA(
MEROPS; S01.269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
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Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xylella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10910347;
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57 POTENTIAL
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                                                                    pathogen
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RESULT
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21595285; PubMed=11759840;
MEDLINE-21595285; PubMed=11759840;
Manage A., Kanage A., Kawashima Matanabe A., Iriguchi M., Ishikawa A., Kawashima Kishida Y., Kohara M., Matsunoto M., Matsuno A., Katsuno A., Katsuno A., Shimpo S., Sugimoto M., Takazawa M.,
                                                                                                                                                                                                                                                                                              Q8YM87
Q8YM87;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2002
                                                                                                                                                                                       Anabaena sp. (Strut...
Racteria; Cyanobacteria;
                                                                                                                                                                                                                                                        ALR5049.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL; AJ305145; CAC27157.1; HSSP; P09331; 1EXF.
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Bacteria; Firmicutes; Baci
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                                                                                                                                                                                                                                                                         Hypothetical protein
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InterPro; IPR00126; Ser_proteas_V8.
Pfam; PF00089; trypsin; or
PRINTS; PR00839; V8PROTEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis extracellular serine proteinase."; ubmitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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les 8; Conserv
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2 (TrEMBLrel. 20, La:
al protein Alr5049.
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llarity 100.0%;
Conservative (
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20, Last sequence update)
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                                                                                                                                                                                                           Nostocales;
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EXTRACELLULAR SERINE PROTEINASE.

FB9B886D453B8BB7 CRC64;
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Pred. No.
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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6.7;
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                          o A., Muraki A.,
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                                                                                                Sasamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 217;
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                                 Q9ZDX8
AC Q9ZDX8
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                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                                                    Q9ZDX8
Q9ZDX8;
01-MAY-1999
01-MAY-1999
01-JUN-2002
Protease DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q47809;
01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases. EMBL; 21295; CAA78168.1; -. IFRO01254; Ser_protease_Try. InterPro; IPRO01254; Ser_protease_Try. InterPro; IPRO0126; Ser_proteas_V8.
PRINTS; PRO0839; V8PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q47809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
EMBL; AP003598; BAB76748.1; -.
                                 SEQUENCE FROM
STRAIN-MADRID
                                                                                                                 Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsi
                                                                                                                                                            Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resembles serine proteinase strain V8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=OG1-10;
Su Y.A., Clewell D.B.;
"A gene (sprE) downstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcal serine proteinase homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                             NCBI_TaxID=782;
                                                                                                                                                                                    RP186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome.
SEQUENCE 169 AA; 17427 MW; 0A610CC04EE4C48A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                      224 TGGQSGSPI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 TGGNSASPV
                                                                                                                                                                                                                                                                                                                                                        œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGNSGSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tabata S.;
                                                                                                                                                              prowazekii.
                                                                                                                                                                                                    (TrEMBLrel.) (TrEMBLrel.) (HTRA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease.
284 AA; 31063 MW;
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5 (TrEMBLrel. 01,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                 E N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                    Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%;
88.9%;
                                                                                                                                                                                                                        10,
10,
21,
                                                                                                                 alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gelE of Enterococcus faecalis OG1-10 determinant of Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D4F0312BEE778415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                               315
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7.8;
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                                                                                                                                                                                                                                                                                                               AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                        Rickettsiales;
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RESULT
Q62313
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Best Local
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                                     DOMAIN
TRANSMEM
                                                                                       Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q62313
Q62313;
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trans-golgi network integral membrane protein TGN38A precursor (Trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -|- SIMILARITY: TO SERINE PROTEASES, T

EMBL; AJ235270; CAA14652.1; -.

InterPro; IPR001478; PDZ.

InterPro; IPR001940; Protease2C.

InterPro; IPR001254; Ser_protease_Try.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Winkler H.H., Kurland C.G.,
                                                                                                                 MGD;
                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                   STRAIN-ICR; TISSUE-BRAIN;
MEDLINE-95301533; PubMed-7540170;
Kasai K., Takahashi S., Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                              golgi network protein 1) (TGN38 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50106; PDZ; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondria.";
Nature 396:133-140(1998)
                                                                           CHAIN
                                                                                                                                        EMBL; D50031;
                                                                                                                                                                                                                                                                                                         "Strain-specific presence of two TGN38 isoforms and absence of TGN41 in mouse.";
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersson S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 TGGASGSPV 196
                                                                                                                                                                                                                                                                                               Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGGNSGSPV 9
                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PRIMARILY IN TRANS-GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND THE CELL SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY). TISSUE SPECIFICITY: WIDELY EXPRESSED.

MISCELLANEOUS: ALSO FOUND IN STRAINS BALB/C, C57BL/6 AND DBA/2.
                                                                                                  L; BC009143; AAH09143.1; MGI:105080; Ttgnl. al; Transmember
                                                                                                                                                                                                                  mitted (JUN-2001) to the EMBL/GenBank/DDBJ databases FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TR. FROM TRANS-GOLGI NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conserv
                                                                                                                                                                                                                                                                                                Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease; Complete proteome. 315 AA; 35033 MW; 2D91A0D54FFBE9A1 CRC64;
18
299
320
346
131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                           18
                                                                                                                                                                                                                                                                                             270:14471-14476(1995).
298
319
353
349
178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.3%;
                                                                                                   Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40;
Pred. No.
           CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY).
                                                 EXTRACELLULAR
                                                                          TRANS-GOLGI NETWORK
                                                               PROTEIN TGN38A
                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prowazekii and the origin
                                                                                                                                                                                                                                                                                                                                    Nakayama K.;
                                                                                                   Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRYPSIN FAMILY.
TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                 (POTENTIAL)
REPEATS
                                                                                                 Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 315;
                                                                           INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                               TRAFFIC TO AND
                                                                           MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of.
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RESULT 10
Q62314
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Best Local S
Matches 7
                   Query Match
Best Local
     Matches
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CARBOHYD
                                                                       REPEAT
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q62314
Q62314;
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REPEAT
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                                                                                                                         REPEAT
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REPEAT
                                                                                                                                                                                                              DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                      Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 270:14471-14476(1995).
-:- FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRAI-FROM TRANS-GOLGI NETWORK.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trans-golgi network integral membrane protein TGN38B precursor (Trans-golgi network protein 2) (TGN38 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95301533; PubMed-7540170;
Kasai K., Takahashi S., Murakami
"Strain-specific presence of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-BRAIN;
                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:105079; Tgoln2
                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
-!- MISCELLANEOUS: NOT FOUND IN STRAINS BALB/C, C57BL/6 AND DBA/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY). TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGNSGKP
Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 87.17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
139
147
155
163
171
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                                                                         AA;
                                                                  308
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148
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                     83.3%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
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2.
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6.
N-LINKED
N-LINKED
                     Score 40;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
ENDOCYTOSIS SIGNAL (BY
7 X 8 AA TANDEM REPEATS
                                                                         N-LINKED (GLCNAC. . .) (P
2826FA9E958C5C27 CRC64;
                                                                                                               7654321
                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                PROTEIN TGN38B.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  TRANS-GOLGI NETWORK
                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                              ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95C340C2F4A21EB3 CRC64;
     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGN38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGULATING MEMBRANE TRAFFIC
                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                   Repeat; Golgi stack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakayama K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. .
                   DB
38;
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                                     11;
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                                   Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 353;
                                                                                                                                                                                                                                                                                                                                    INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIMARILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               absence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
                                                                                                                                                                                                                                                                                                                                    MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of TGN41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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   Gaps
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TGGNSGSP

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RESULT
Q8VA04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 8
                                Komorowska B., Malinowski T.;

"Diversity of the coat protein gene sequence of several ASI isolates.";

I isolates.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. Results, AF438521; AAL32457.1;

R InterPro; IPR001899; Gram_pos_anchor.

R InterPro; IPR001052; pltvir_coat.

R InterPro; IPR000052; pltvir_coat.

R Pfam; PF00286; virus_p-coat; 1.

R Pfam; PF00286; virus_p-coat; 1.

R PFRNITS; PR00232; POTXCARLOAT.

R PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

R PROSITE; PS003418; POTEX_CARLAVIRUS_COAT; UNKNOWN_1.

R PROSITE; PS003418; POTEX_CARLAVIRUS_COAT; UNKNOWN_1.

SEQUENCE 396 AA; 42574 MW; E92377805EBBC333 CRC64;
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q92J35;
Q92J35;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8VA04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8VA04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00595; PDZ; 1. Pfam; PF00089; trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE008590; AAL027/2.1; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogata H., Audic S.,
Samson D., Roux V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mechanisms of evolution in Rickettsia Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MALISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsiaceae;
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alp. Rickettsiaceae; Rickettsiaceae;
                                                                                                                                                                                                                                                                                                                  STRAIN-MT32;
                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA
                                                                                                                                                                                                                                                                                                                                                                                                                            Apple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=35350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGNSGKP
                                                                                                                                                                                                                                                                                                                                                                                                                            stem pitting virus
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00089; trypsin; 1.
PS50106; PDZ; 1.
; Complete proteome.
497 AA; 55517 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                   positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cossart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Renesto-Audiffren P.,
Cossart P., Weissenba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%;
88.9%;
    81
    . 28;
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19,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
  Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4EB5872B552EFC6C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
53;
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  DB
                                                                                                                                                                                                                                                                                                                                                                                                     no DNA stage; Foveavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fournier P.-E., Barbe
ch J., Claverie J.-M.,
  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 497;
Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽.
                                                                                                                                                                                                                                                                   ASPV
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RESULT 14
Q9P7S1
ID Q9P7S
AC Q9P7S
DT 01-OC
DT 01-U
DE Hypot
GN SPACZ
OS SCALZ
OC SCALZ
OC SCALZ
OX NCBIL
RN [1]
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Q9LK70
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Best Local
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabi
Sequence features of the regi
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP000373; BAB01154.1;
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LK70
Q9LK70;
Q9LK70;
Q1-QCT-2000 (TrEMBLrel. 15,
Q1-QCT-2000 (TrEMBLrel. 15,
Q1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity to serine protease.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                  Schizosaccharomyces pombe (fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                              O9P7S1 PRELIMINARY; PRT; 996 AA.

O9P7S1,

O1-CCT-2000 (TrEMBLrel. 15, Created)

O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)

O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Hypothetical signalling-associated PDZ domain containing

SPAC23G3.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00834; PROTEASES2C PRINTS; PR00839; V8PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00595; PDZ; 1. Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00228; PDZ;
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                                                                                                                                                                                                                                                                                                                                                                                         219
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IPR001254; Ser_protease_Try.
IPR000126; Ser_proteas_V8.
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499 AA;
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Search completed: December 20, 2002, 12:10:22 Job time: 52.3158 secs
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C 074325;
T 01-NOV-1998 (TrEMBLrel. 08, Created)
T 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 111.3 kDa protein C1685.05 in chromosome II.
S PBC1685.05.
S Chizosaccharomyces pombe (Fission yeast).
S Chizosaccharomyces pombe (Sission yeast).
C Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
C Schizosaccharomyces.
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CSTRAIN-972H-;

RA Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;

RA LSubmitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL138854; CAB72237.1; -.

InterPro; IPR00114; HPT_SerP_site.

InterPro; IPR001478; PDZ.

R InterPro; IPR001940; Protease2C.

PFam; PF00595; PDZ; 1.

RPAINTS; PR00834; PROTEASES2C.

RR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.

SEQUENCE 996 AA; 110407 MW; A008E51746B05AC3 CRC64;
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Best Local S
Matches 7
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Best Local S
Matches 7
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-! -SIMILARITY: TO YEAST YUL123W.
EMBL; ALO31154; CAA20053.1; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR00124; Ser_Protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00228; PDZ; 3.
PROSITE: PF500240; TRYPSIN_DOM; 1.
Hypothetical protein.
SEQUENCE 997 AA; 111292 MW; D32D7E3CCAE877AO CRC64;
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227 SGGSSGSPV 23:
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77.8%;
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Pred. No. 1.6e+02;
2; Mismatches 0; Indels
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Pred. No. 1.6e+02;
2; Mismatches 0; Indels
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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4: /cgn2_6/ptodata/
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-221-0178-1045
US-09-058-411-1
US-09-134-001C-1520
                  US-09-441-340-2
US-09-454-721A-3
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equence 97, App	Sequence 6, Appli	equence 5, Appl	equence 5, Appl	e 5, Appl	equence 5, Appl	equence 5, Appl	2,	5, Appl	4, Appl	e 16, Āpp	e 8, Appl	7, Appl	equence 7, Appl	equence 7, App	1, Appl	equence 7, Appl	Œ	equence 7, Appl	equence 7, Appl	ω,	equence 3, Appl	e 1, Appl	e 1,	e 4,	equence 4,	equence 1,	equence 1,	e 50	equence 5	equence 9,	•

RESULT 1 US-09-221-017B-726 Sequence 726, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION: NUMBER OF SEQUENCES. CORRESPONDENCE ADDRESS: ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto CA CA CITY: CA APPLICATION NUMBER: PP1182: FILING DATE: 31-DEC-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: PP1546 FILING DATE: 30-JAN-1998 SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: US/09/221,017B FILING DATE: 30-JAN-1550 PRIOR APPLICATION DATA: PRIOR TARTON NUMBER: PP2911 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette PRIOR APPLICATION DATA: TITLE OF INVENTION: NUMBER OF SEQUENCES: FILING DATE: 2 CLASSIFICATION: COMPUTER: IBM CON OPERATING SYSTEM: COUNTRY: USA ZIP: 94304-1018 ROSS, Bruce C. P. GINGIVALIS NUCLEOTIDES AND USES THEREOF 23-DEC-1998 Compatible Windows

APPLICATION NUMBER: FILING DATE: 09-APR-PRIOR APPLICATION DATA:

09-APR-1998

APPLICATION NUMBER:

10-DEC-1998

PCT/AU98/01023

ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-221-017B-726
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1696
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                 1636
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LENGTH: 1974 base pairs
             180 lnCysProArgLeuIleGlnGluLeuLysLeuIle 191
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TELEX: 706141
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STRANDEDNESS: double
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                                                                                                                                               lyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspL 160
                                                                                                                                                                                                                  snAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleG 140
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                                                               TGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGACAAATGGGGTC
                                                                                 euGlnArgThrIleSerValAspIleArgTyrValLeuPheMetIleAspLysTrpGlyG
                                                                                                                               GTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATC
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AGTGCCCCCGTCTCATCCAAGAGCTGAAGTTGATC 1730
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US-10-008-355-2_COPY_522_712 (1-191) x US-09-221-017B-1045 (1-2384)
                                                                                                    Best Local Similarity:
Query Match:
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MOLECULE TYPE: DNA (Y-
HYPOTHETICAL: NO
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
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APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PP29
FILING DATE: 09-APR-1998
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FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 32.
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
22 IleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 755 PAGE CITY: Palo Alto
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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GENERAL INFORMATION U.
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               FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: WHITE JR, PAUL E
REGISTRATION NUMBER: 32011
REFERENCE/DOCKET NUMBER: 3133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                    ZIP: 2000 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: FLOOS/MS-DOS
COMPUTER: FLOOS/MS-DOS
FC-DOS/MS-DOS
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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STREET: 11
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                                                                                                                                                                                                     APPLICATION NUMBER: US/09/01
FILING DATE: April 10, 1998
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                                                                                                                                                    APPLICATION NUMBER: BR 9701774.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCGCAGCATCATTGT\GATATTCGCTACGTCCTGCTTGTGATAGACAAAGTAGGCGGT 593
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                                                                                                                                                                                                                                                                                                                                                                                                   D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                     E: CUSHMAN DARBY & CUSHMAN

E: Intellectual Property Group of

E: PILLSBURY MADISON & SUTRO LLP

1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALLER, Ricardo
VENTION: VACCINES AGAINST INFECTIONS CAUSED BY YF
VENTION: VITUS; YF INFECTIOUS CDNA, METHOD FOR PRODUCING
VENTION: RECOMBINANT YF VIRUS FROM THE YF INFECTIOUS CDNA
VENTION: PLASMIDS TO ASSEMBLE THE YF INFECTIOUS CDNA
                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                   NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1520
LENGTH: 1083
TYPE: DNA
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                Sequence 1520, Application US/09134001C
                                                                                      CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID TITLE OF INVENTION: EPIDERMIDIS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
ORGANISM: Staphylococcus epidermidis
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ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: sing
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Indels:
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US-09-134-001C-1520

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; NAME/KEY: mat_peptide
; OTHER INFORMATION: nuo
US-09-660-587-3
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                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09660587 Patent No. 6392023 GENERAL INFORMATION:
                                                                                                                                                                                       SEQ ID NO 3
LENGTH: 849
TYPE: DNA
ORGANISM: Ehrlichia canis
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/261,358
PRIOR FLUING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                APPLICANT: Yu, Xue-Jie TITLE OF INVENTION: Homologous 28-kilodalton TITLE OF INVENTION: Genes of Ehrlichia canis FILE REPERENCE: D6152CIP2 CURRENT APPLICATION NUMBER: US/09/660,587 CURRENT FILING DATE: 2000-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAAGGGGCGCATCCCATGAAAAACATCAAGAAACCCTTTGATTTAAAAGGTAAGTCA 117
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Indels:
Gaps:
                                Conservative: Mismatches:
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FILE REPERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR ETLING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 3
LENGTH: 849
TYPE: DNA
ORGANISM: Ehrlichia canis
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                                                   US-10-008-355-2_COPY_522_712 (1-191) x US-09-261-358A-3 (1-849)
                                                                                                      Query Match:
                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                          Score:
                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                 US-09-261-358A-3
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US-09-261-358A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Walker, David
APPLICANT: WcBride, Jere
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Home
TITLE OF INVENTION: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09261358A Patent No. 6403780
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                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
OTHER INFORMATION: nu
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39.38%
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Genes of Ehrlichia canis
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Query Match:
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                                                                                                                                                         US-10-008-355-2_COPY_522_712 (1-191) x US-08-990-823-39 (1-841)
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                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 49086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 39, Application US/08990823D Patent No. 6228371
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: US 96/10375
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,254
EARLIER FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/990,823D CURRENT FILING DATE: 1997-12-15
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 841
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                 PEATURE: Modified base
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                                                             GlySerIleLysGlyTyrGluProGlnAsp----
                                                                                                                           MetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArg---MetSerTyr
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77.50
32.91%
25.32%
7.73%
-GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyVal 77
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Matches:
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US-09-103-840A-2
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APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                    US-10-008-355-2_COPY_522_712 (1-191) x US-09-103-840A-2 (1-4403765)
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Best Local Similari
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APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                             205591
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                                                     205651 AGCAACTACAAAATCCCCGTCGATGCCTCGGCGAACGTGCATTCGGTGTCA-----
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OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4403765
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LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu
                                                                                                                           GGCAAGGTTACTGCCGTCGAGCCCACCGACCAGGGCGCACGAGTGACGATGAGCATCGCC
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRATITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                                   205562 GTGTCCACCGGTGCTCCGGGTAAATACTTCTCCTCCGGACAG-----
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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 SerAsnAsnAspIleThrGlyGlyAsnSerGlySer--
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                                                                                    PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeu 117
                                                                                                                                                        LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu 97
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US-09-454-721A-3
; Sequence 3, Application
; Patent No. 6296854
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: Sequence 2, Application US/09441340

: Patent No. 6448476
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APPLICANT: Peter Pushko
APPLICANT: Michael D. Parker
APPLICANT: Jonathan F. Smith
APPLICANT: Burce J. Crise
TITLE OF INVENTION: Live Attenuated Venezuelan
FILE REFERENCE: Army 146
CURRENT APPLICATION NUMBER: US/09/454,721A
CURRENT FILING DATE: 1999-12-07
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CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
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TITLE OF INVENTION: Phosphonate Metabolizing
FILE REFERENCE: 38-21(15303)
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75.00
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PRIOR APPLICATION NUMBER: US

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                        Sequence 9, Application US/08433522A Patent No. 6013514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 3
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                                                                                                                                                                                                     GENERAL INFORMATION:
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ORGANISM: Venezuelan Equine Encephalitis Virus
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APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                                                       APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
                                                                                                                                                                                                                                                                                                                   8363 ACTCCGGAG 8371
                                                                                                                                                                                                                                                                                                                                                                                        8303 GGATCTAGGACAGCCCTTTCAGTCGTCATGTGGAACGAGAAGGGAGTTACCGTGAAGTAT 8362
                                                                                                                                                                                                                                                                                                                                                                                                                                                             8192 AATGGGCGTTTCACGGTG------CCGAAAGGAGTTGGGGCCAAGGGAGACAGCGGA 8242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8132 TACACCCATGAGAAACCCCCAAGGCTATTACAGCTGGCATCATGGAGCAGTCCAATATGAA 819:
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                                                       NUMBER OF SEQUENCES:
                                                                        TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7952 ATGTTGGAAGGGAAGATAAACGGCTACGCTTGTGTGGTCGGAGGGAAGTTATTCAGGCCG 801:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 ProGlyArg-------AlaLeuProSerAspAlaAsnPheThrMetArg
                                                                                                                                                                                                                                                                                                                                                    GluProAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProLysSerAsp---GluPheAla---ValGlnGluAsnIle---LeuAspLeuPheArg 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCATGTGGAAGGCAAGATCGACAACGACGTTCTGGCCGCGCTTAAGACGAAGAAAGCA 8071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGly-----
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Best Local Similarity:
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TELEFAX: (416) 595-163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2989 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,52
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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1761 ACGAAAAATGATTATGGTACGAGTGTCAATTTGGGTTATACCGAACCCTATTTTACTAAA 1820
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STATE: Ontario
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                                                                  GATCCTATCAATGGTAGCAATGAAGAAGTGGATGTCGTATATAAAGTCAAAGAACGTAAC 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                      MetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGly 55
                               LeuSerAsnAsnAspIleThrGlyGlyAsnSerGly----SerProValPheAspLys 134
                                                                                                                                                                                                                                   Asp-----
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                                                                                                                                   ACGGGTAGTATCAACTTTGGTATTGGTTACGGT-----ACAGAGAGTGGTATCAGTTAT 1700
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Conservative:
Mismatches:
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                                                                                                                        Percent Similarity:
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GENERAL INFORMATION:
APPLICANT: CHONG,
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                                                                                                                                                       NO . .
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2989 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 12-SEP-
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
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16 MetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGlu 35 :::||| ::: ||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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LOOSMORE, Sheena
SIA, Dwo Yuan Charles
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US-08-942-046-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application Patent No. 6264954
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCE ADDRESS;

CORRESPONDENCE ADDRESS;

Sim & McBurney

Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: APPLICANT:
                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,04
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1848 TTCTTTGAA 1856
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             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                     MSG 1R7
STEWART, Michael I
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                                                                                                                                                                                                                                                                                                            Ontario
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SIA, Dwo Yuan Charles
KLEIN, Michel
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YANG, Yan Ping
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                                                                                                                                             US/08/942,046
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REFERENCE/DOCKET NUMBER: 24,

24,973

1038-732 MIS:jb

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US-09-206-942-52; Sequence 52, Application; Patent No. 6432669; GENERAL INFORMATION:
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Best Local Similarity:
                                                                            RESULT 15
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TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2989 base pairs
APPLICANT: Loosmore, Sheena
                                                                                                           1848
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LOCATION:
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TOPOLOGY: lir
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                                                                                                         TTCTTTGAA 1856
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                                                                                                                                                                                                                                ACGAAAAATGATTATGGTACGAGTGTCAATTTGGGTTATACCGAACCCTATTTTACTAAA 1820
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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Best Local Similarity:
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SEQ ID NO 52
LENGTH: 2934
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High TITLE OF INVENTION: Molecular Weight Proteins FILE REPERENCE: 1038-861 MIS:jb CURRENT APPLICATION NUMBER: US/09/206,942 CURRENT FILING DATE: 1998-12-08 EARLIER APPLICATION NUMBER: 09/167,568 EARLIER FILING DATE: 1998-10-07 NUMBER: 09/167,568 EARLIER FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
      946
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                                                                                                                  IleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluPro
                                                                                                                                                                                                                                                         ArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSer 118
                                                                                                                                                                                                                                                                                                                                                                                       TCCAGTGATTCACGAAGTTTTGCGGGGAGTAAAGTTCCAC-----GGCAAGAAT-----
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GGCTCTAATCTTACCTTAAATTCCCCATGTTCGCAAGTATAATGCTTTTGAAATCAATAAA
                                      AspLeuGlnArgThrIleSerValAspIleArg---TyrValLeuPheMetIleAspLys 177
                                                                                TGGGGT----
                                                                                                                                                        AATATTTCGGTCACTGGCGGA-----GGTTCTGTGTTTTTCGATATATACGCTAACCTT
                                                                                                                                                                                          {\tt AsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeu}
                                                                                                                                                                                                                                    AGGTTAAAACCAAATGAGAAGACAACTCCTAACAGACCACTACCAATTCAGTTTTTATCT
                                                                                                                                                                                                                                                                                                                                                 {\tt GluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPhe}
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73.50
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Matches:
Conservative:
Mismatches:
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Search completed: December 21, Job time: 2265 secs 2002, 02:28:25

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OM protein - nucleic search, using frame_plus_p2n model
                                                December 21/
                                                                                                                                                Copyright
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2002, 01:47:03; Search time 2159 Seconds (without alignments)
1432.764 Million cell updates/sec
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Compugen Ltd.
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Scoring table: Perfect score: Sequence: Title: US-10-008-355-2_COPY_522_712 1003 1 SKSVIAAARNIQADAMANAY..... BLOSUM62 .LFMIDKWGQCPRLIQELKLI 191

Searched: Xgapop 10.0 , X Ygapop 10.0 , X Fgapop 6.0 , F Delop 6.0 , I 16154066 seqs, 8097743376 residues Xgapext Ygapext Fgapext Delext 0.5 7.0 7.0

Minimum DB Maximum DB Total number of hits satisfying chosen parameters: seq length: 0 length: 2000000000

32308132

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEY=xlh
-Q-cgn2_1/USPT0_spool/US10008355/runat_17122002_112705_16942/app_query.fasta_1.327
-Q-cgn2_1/USPT0_spool/US10008355/runat_17122002_112705_16942/app_query.fasta_1.327
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPELT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAN>100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UTFMT=pto -NORM=ext -HEAP\$;IZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_eCGN_1_1_763_@runat_17122002_112705_16942 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1; -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : em_gss_fun:*
em_gss_mam:*
em_gss_mus:* gb_est2:*
gb_htc:*
gb_est3:* gb_est1:* em_estro:* em_estpl:* em_estov:* em_estmu:* em_esthum: * em_htc:* em_estin:* em_estba:* em_gss_hum:*
em_gss_inv:* em_gss_other:*
em_gss_pro:* em_gss_pln:* em_estom:* gb_est5:* gb_est4:* em_gss_vrt:* gb_gss:* em_estfun:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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872 829 811 825	BH400391 AG-ND-147 BH4701391 AG-ND-147 BH371846 AG-ND-162 BH371846 AG-ND-162 BH371846 AG-ND-162 BH371846 AG-ND-162 BH37184 AG-ND-162 BH391629 602535962 B1391728 pgpln.pk0 BE268652 601125126 BM838106 K-EST0114 BQ215538 AGENCOURT BR799506 601589315 BM465284 AGENCOURT BM44938 AGENCOURT BM44938 AGENCOURT BM652808 AGENCOURT BM91758 AGENCOURT BM928590 AGENCOURT BM928590 AGENCOURT BM928590 AGENCOURT BM928590 AGENCOURT BM91788 AGENCOURT BM91788 AGENCOURT BM91788 AGENCOURT BM91780 AGENCOURT BM91778 AGENCOURT BM91778 AGENCOURT BM91778 AGENCOURT BM91778 AGENCOURT BM91778 AGENCOURT BM91778 AGENCOURT BM909854 AGENCOURT BM909857 AGENCOURT BM909854 AGENCOURT BM6091879 602819275 BG649391 AGENCOURT BM64132 Homo sapl BG6449391 AGENCOURT BM641384 RC2-HT107 AU131725 AU131725 AU134050 AU134050 B1116059 60286455 BQ692534 AGENCOURT BG692634 BEST501733 B1334196 602997681	

ALIGNMENTS

AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	вн400391/с	RESULT 1
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.	1 (bases 1 to 426)	Anopheles.	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Anopheles gambiae	African malaria mosquito.	GSS.	BH400391.1 GI:17346607	BH400391	DNA sequence.	AG-ND-147H4.TF ND-TAM Anopheles gambiae genomic clone AG-ND-147H4,	BH400391 426 bp DNA linear GSS 11-DEC-2001		

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RESULT 2
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                                                            AGACTTATAGGTCTTGCATTTGACGGAAACAGTGAAGCT 1
                                                                                ArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAla 149
                                                                                                                                             LeuSerAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGly 136
                                                                                                                                                                                         TATAAAAAGAAAATTATGGTATGTACAAAGACAAAGACGGGCAACTTCATGTAAACTTC
                                                                                                                                                                                                          PheArgThrLysAsnTyrGlyArgTyrAlaGlu----AsnGlyGlnLeuHisIleAlaPhe 116
                                                                                                                                                                                                                                                                                    LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu
                                                                                                                                                                                                                                                                                                                                               LysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyVal 77
                                                                                                                                                                                                                                                                                                                                                                                 TATCCGGATGCTAACTCTACGATCAGGTTAACTTATGGTCAGATCGAGACGCTTCCTAAA
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Seq primer: M13
Class: BAC ends
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 977
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Other_GSSs: AG-ND-147H4.TR
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/clone="AG.ND-147H4"
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/note="Vector: pECBAC1; Site_1:
79 c 76 g 160 t
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                                                                                                                                                             ACTITAGIA 130
                                                                                                                                                                                                                                                                                ArgTyrValLeuPheMetIleAspLysTrpGlyGlnCysProArgLeuIleGlnGluLeu 188
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AGENCOURT_6597467 NIH_MGC_41
5', mRNA sequence.
BM562210
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This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from meters of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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Shetty,J., Malek,J., Koo,H.,
Direct Submission of BAC-end
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Eukaryota; Metazo
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BM562210.1
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/note="Vector: pECBAC1; Site_1:
142 c 155 g 290 t
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/strain="PEST"
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                                                              111 GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly-----
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                                                                                                                                                                      GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                             ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium of DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informatic
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/lab_host="hHl0B (phage-resistant)"
/note="forgan: skin: Vector: poTBP; Site_1: XhoI; Site_2:
/note="forgan: skin: Vector: poTBP; Site_1: XhoI; Site_2: Vector: poTBP; Site_2: Vector: poTBP; Site_1: XhoI; Site_2: Vector: poTBP; Site_1: 
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/clone="IMAGE:5480814"
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                                                                               19 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
39 GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet--
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                                       AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC
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1 (bases 1 to 630)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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602535962F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:4684958
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                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="amelanotic melanoma, cell line"
/lab_host="PH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTBF; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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155 c 177 g
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/db_xref="taxon:9606"
/clone="IMAGE:4684958"
/clone_lib="NIH_MGC_41"
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MENT	FEREN AUTHO FITLE	ACCESSI VERSION KEYWORD SOURCE ORGAN	RESULT BI39172 LOCUS DEFINIT	Db 5	Qy 1	Qy 1 Db 4	Qy 1 Db 4	Qy 1 Db 3	Qy Db 3	Qу Дъ з	оу	Db 2
, AL	S S S	NON .	HON 8		64							207
Unpublished (2001) Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1335 Fax: 302-831-2822 Email: cogburn@udel.edu, www.chickest.udel.edu.	s.) gburn,L.A. ed Chicken Animal Gen	coiled-coil containing protein 2 [Mus musculus], mRNA sequence. BI391728.1 GI:15085010 EST. chicken. Gallus gallus Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	BI391728 667 bp mRNA linear EST 06-AUG-2001 pgpln.pk005.f8 Normalized Chicken Pituitary/Hypothalamus/Pineal Library Gallus cDNA clone pgpln.pk005.f8 5' similar to	TGCGCAGTGGAGTTCAACTTC 551	IleSerValAspIleArgTyr 170	ASPG1YASnTrpG1uA1aMetSerG1YASpI1eG1uPheG1uProAspLeuG1nArgThr 163 :::	GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143 	GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly	GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGly 110 ::: ::::: AGCCGGTTTGAAAACTACGGAGACAAGTTTGCAGAG 377	ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91 CGCACTGGGAAG	SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71 ,	:::
	AL Unpul Conta Unive Town: Tel: Fax: Emai	laaninae; Gallus. bases 1 to 667) bases 1 to 667) er,T.E. and Cogburn,L.A. from Normalized Chicken ary USDA/IFAFS Animal Gen ary USDA/IFAFS Animal Gen blished (2001) act: Larry A. Cogburn act: Larry A. Cogburn ersity of Delaware send Hall, Newark, DE 197 302-831-1335 302-831-1335 302-831-2822 1: cogburn@udel.edu, www.	coiled-coil containing protein 2 [Mus musculus], mRNA seque ON BI391728.1 GI:15085010 S EST. chicken. ISM Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. CE 1 (bases 1 to 667) RS Porter T.E. and Cogburn, L.A. ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal library USDA/IFAFS Animal Genome Project AL Unpublished (2001) Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1335 Fax: 302-831-2822 Email: cogburn@udel.edu, www.chickest.udel.edu.	BI391728 BI391728 BI391728 Inear EST 06-AUG- pgpln.pk005.fB Normalized Chicken Pituitary/Hypothalamus/Pineal Library Gallus gallus cDNA clone pgpln.pk005.f8 5' similar to gb hAAH04057.llAAH04057 (BC004057) Similar to transforming, acid coiled-coil containing protein 2 [Mus musculus], mRNA sequence. BI391728.1 GI:15085010 EST. Chicken. Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Archosauria; Aves; Neognathae; Galliformes; Phasianidae; phasianinae; Gallus. 1 (bases 1 to 667) Porter, T.E. and Cogburn, L.A. ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA Library USDA/IFAFS Animal Genome Project Unpublished (2001) Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-2822 Email: cogburneudel.edu, www.chickest.udel.edu.	HI391728 BI391728 BI391728 BI391728 BI391728 BI391728 DIARRON PURINCH PILLITARY/HYPOTHALAMUS/Pineal CLIDRARY Gallus gallus CDNA clone pgpln.pk005.f8 % similar to transforming, acid coiled-coil containing protein 2 [Mus musculus], mRNA sequence. BI391728.1 GI:15085010 EST: Chicken BI4391728 BI4391728 BI391728.1 GI:15085010 EST: Chicken Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 667) POTTER, T.E. and Cogburn, L.A. ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA library USDA/IFAFS Animal Genome Project Unpublished (2001) Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-3822 Email: cogburn@udel.edu, www.chickest.udel.edu.	IleServalAspIleArgTyr 170 ::: ::: TGCGCAGTGGAGTTCAACTTC 551 B1391728 B1391728.1 G1:15085010 EST. Chicken. EST. Chicken. B1391728.1 G1:15085010 EST. Chicken. B1391728.1 G1:15085010 EST. Chicken. B1391728.1 G1:15085010 EST. Chicken. B1391728.1 Chicken. B1391728.1 G1:15085010 EST. Chicken. B1391728.1 Chordata; Craniata; Vertebrata; Euteleostom Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 667) Porter, T. E. and Cogburn, L.A. ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA 11brary USDA/IFAFS Animal Genome Project Unpublished (2001) Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-3822 Email: cogburn@udel.edu, www.chickest.udel.edu.	AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163	GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143	GinLeuHisTleAhlaPheLeuSerAsnAspAieThrCly	GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGly 110	ThrThrGlyLysGlyValLeuGluLysGlnAspProtysSprAspGluPheAlaValGln 91 GGCACTGGGAAG	SerTyrGlySerITeLysGlyTyrGlubroGlnAspGlyAlaTrpTyAsnTyHis 71

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGly 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGly 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLysSer 85
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 701)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
Plate: LLCM132 row: c column: 07
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/lab_host="DH10B (phage-resistant)"
/lnote="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC-----TATGGCTATGGA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAATCCAGAAGGAAGCCTTGGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AACGATGTGATTGGCTGCTTTGCGGATTTTGAA 397
                                  Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                      Eukaryota;
Mammalia;
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BM838106
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Frontier Korean EST Project 2001
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                                                                                                  Eutheria;
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                                       111 GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly-----
                                                                                                                                                                                                                                                                                                                                                           175 GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
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                                                                                                                                                                              286 GGCACTGGGAAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                                                                                                                                                                                      ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC 174
                                                                                                                                GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: yongsung@mail.kribb.re.kr
Plate: 73 row: C column: 05
High quality sequence stop: 710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Research Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note "organ: Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (FAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into DraIII- digested pME185-FL3 vector. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method The cDNA libraries constructed by this method are full-length enriched cDNA library."

182 c 201 g 164 t
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/cell_line="SNU-601"
/lab_host="Top10F'"
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/clone_lib="S9SNU601"
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/db_xref="taxon:9606"
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                                        39
GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                    GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet------
                                                                             AGCTATGGGGTCAGAAGGGGCCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC 162
                                                                                                                    AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM13284 row: c column: 14
High quality sequence stop: 673.
Location/Qualifiers
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B0215538
B0215538.1 GI:20396938
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="PH10B (phage-resistant)" cell line"
/lab_host="Ph10B (phage-resistant)" cell line"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally: oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 228 c 239 g 186 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM798 row: n column: 03
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Mammalia; Eutheria;
1 (bases 1 to 853)
                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 24 High quality sequence stop: 790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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National Institutes of Health, M
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        202
/note="Organ: lung; Vector: pOTBT; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 203 c 255 g 193 t
                                                                                                                                                                                                               /clone_lib="NIH_MGC_7"
/tissue_type="small_cell_carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                               /clone="IMAGE:3943490"
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Primates;
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Catarrhini;
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i; Hominidae; Homo.
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AGENCOURT_6409930 NIH_MGC_85
5', mRNA sequence.
BM456284
BM456284
BM456284.1 GI:18505324
EST.
                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informat:
                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 881)
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                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                  Unpublished (1999)
http://image.llnl.gov
            found through the I.M.A.G.E. Consortium/LLNL at:
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US-10-008-355-2_COPY_522_712 (1-191) x BM456284 (1-881)
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Best Local Similarity:
899 b,
N AGENCOURT_6392962 NIH_MGC_72 H
5', mRNA sequence.
BM449938
BM449938.1 GI:18498978
EST.
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/tissue_type="lymphoma, cell line"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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/db_xref="taxon:9606"
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Tissue Procurement: ATCC/DCTD/DTP
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Plate: LLAM12205 row: o column: 15
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6;
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US-10-008-355-2_COPY_522_712 (1-191) x BQ645307 (1-904)
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                                                                                                                                                                                                                19 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                                       GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                                                                                                  GlyArgAlaLeuProSerAspAla-
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                                                                                                                                                                   AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC 298
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BQ645307
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EST.
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Plate: LLCM2447 row: j column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 904)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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AGENCOURT_8302363 NIH_MGC_100
-SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="organ: liver; Vector: pOTB?; Site_1: xho1; Site_2: ECCRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/xhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library."
227 c
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/lab_host="DH10B (phage-resistant)"
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Indels:
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He IMAGE:6271209
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 using II RT Librar 222 a 24	BASE COUNT ORIGIN
 /clone_lib="NIME_6598491" /clone_lib="NIME_6598491" /clone_lib="NIME_6598491" /tissue_type="hepatocellular carcinoma, cell line" /tissue_type="hepatocellular carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /lab_host="DH10B (phage-resistant)" /note=""Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:	
	FEATURES Source
cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Apencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	,
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: CGAP (Stanford)	COMMENT
 NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	AUTHORS TITLE JOURNAL
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 942)	ERENCE
 human. human sapiens	SOURCE
 BQ652808.1 GI:21776980	VERSION
	LOCUS DEFINITION
	RESULT 13 BQ652808
TGCGCAGTGGAGTTCAACTTC 643	623 T
IleSerValAspIleArgTyr 170	164 1
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	1 4 4
GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143	
 AACGATGTGATTGGCTGTTTGCGGATTTTGAA 502	470 -
GlnLeuHisIleAlaPh¢LeuSerAsnAspAspIleThrGly 124	111 6
GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGly 110	92 0
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                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10254 row: b column: 06
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus-
1 (bases 1 to 943)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BG174574
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High quality sequence stop: 656.
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                                                          ACCESSION
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                                                                                                                                                                TGTGCTGTGGAATTTAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
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                                                                                                                                                                                                                                                  AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                                                                                                                                              ---GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
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                           5', mRNA sequence.
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BQ646879.1 GI:2177
EST.
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                                                                     AGENCOURT_8342919 NIH_MGC_100
5', mRNA sequence.
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226 c 280 g 209 t
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/dev_stage="10 months, virgin"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro 38
                                                                                                                                                               GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly------
                                                                                                                                                                                                                                                               GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet-----
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D
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-GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/lab_host="PHH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Result
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-Q=/cgn2_1/USPTO_spool/US30008355/runat_17122002_112705_17000/app_query.fasta_1.327
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US10008355_@CGN_1_1_21_@runat_17122002_112705_17000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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10 US-09-815-242-8179
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Sequence 1, Appli
Sequence 525, App
Sequence 4296, Ap
Sequence 8179, Ap
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US-10-008-355-1
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ALIGNMENTS

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Sequence 1, Application US/10008355

Sequence 1, Application US/10008355

Patent NO. US20020164759A1.

GENERAL INFORMATION:
APPLICANT: "Marxis...James
APPLICANT: Potempa, Jan S
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR APPLICANT: Potempa, 355

COURSENT FILING DATE: 2000-11-08

NUMBER OF SEQ ID NOS: 2

PRIOR APPLICANT: Potempa, 355

COURSENT FILING DATE: 2000-11-08

NUMBER OF SEQ ID NOS: 2

PRIOR APPLICANT: Potempa, 355

COURSENT FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: US 60/246,827

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                                                                                                                                                                                                                                                                                   US-09-770-149-525
                                                                                                                                                                                                                                                    Sequence 525, Application Patent No. US20020059663A1 GENERAL INFORMATION:
                                                                                APPLICANT
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences (
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
                                                              APPLICANT:
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                                                                                                                        Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                        Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                       Allen, Keith
                                                                                Davis, Keith R.
                                                                                                                                                                              Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                           Hamilton, Carol M. Price, Jennifer L.
                                                                                                                                                                                                                                An, Yong-Qiang
                                                                                                                                                                     Page, Amy
                                                                                                                                                                                                                                                                         Application US/09770149
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FEATURE:

NAME/KEY misc_feature

LOCATION: (1)...(651)

OTHER INFORMATION: n = A

US-09-770-149-525
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Best Local Similarity:
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                                                                        APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Fa
SEQ ID NO 525
LENGTH: 651
TYPE: DNA
                                                                                                                                                                                                                              Sequence 4296, Application Patent No. US20020061569A1 GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Ess
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
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                                                                                              Carr, Grant J.
Yamamoto, Robert T.
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Indels:
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Conservative:
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CURRENT FILING DATE: 2001-03
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-03-21

2001-03-21

60/206,848 60/191,078

PRIOR

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RESULT 4
US-09-815-242-8179
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA ; ORGANISM: Staphylococcus aureus US-09-815-242-4296
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Sequence 8179, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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LENGTH: 720
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SOFTWARE: FastSEQ for Windows Version
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FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
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APPLICATION NUMBER; 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                     SerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe-----
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                                                                                                                                                                                                                                                                                                                                                                                                        CATGAGTCAACTGGTCCTGTGATGTCAGTAGAAGGTAGCAGCATTGTATATTCAGCGCAT 561
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Query Match:
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Pred. No.:
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: FastSEQ for
SEQ ID NO 8179
LENGTH: 765
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
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APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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LOCATION: (1)
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ORGANISM: Staphylococcus
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679
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364 TATCCAGGTAAAGAAGATGTATCAGTTCAAGTTGAAGAGGGTGCAATAGAACGTGGT
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GTAAAAATGATGACAACAGAAATGCATATGGC----
                               -----AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeu 160
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APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION UMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2020
LENGTH: 1812
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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DB:
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TGTGGTCTCTTAATGCGCCATGAAGTTCTCCGACTC----
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                                                                                                                                                                                                                                                                                         AGTCCTAACGAAGCCATCCTCTGCTCCGACTCGTCCCAAAGCATGTATGCTCAAATGCTA 645
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                                                                       GCTCGTGATATCTCAACCGGAACCCTAAGTTCTCGAATCTTCGATCCTGCCATTAAAAAAC 807
                                                                                                                                                                              TyrAlaGluAsnGlyGlnLeuHis---IleAlaPheLeuSerAsnAsn------
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Indels:
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Best Local Similarity:
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TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2/D1
CURRENT APPLICATION UNMBER: US/10/062,624
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 09/660,587
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 3
LENCTH: 849
TYDEN: NAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Walker, David H. APPLICANT: McBride, Jere W. APPLICANT: Yu, Xue-Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide
OTHER INFORMATION: nuc
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                  AlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSerGlySerPro-----
                                                          TATGAAGCATTTGATGTGAAAAATCCAGGTGATAATTACAAAAACGGTGCTTACAGGTAT 423
                                                                                       LeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIle 114
                                                                                                                                                                          LysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIle 94
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                                                                                                                                        AGTCCAAGAATAGAA-
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Query Match:
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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
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No.:
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SerGlyAspIleGluPheGluProAspLeuGlnArg 162
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                                   CCGACGGCG---GACGGCAAAACCGTTCCGTTCGTGCCGGGAAAAACGTGG------
                                                                          GlyLeuAlaPheAspGly---
                                                                                                                                               AsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIle 139
                                                                                                                                                                                      TCAGGCGGAAAAGGACTCCTTCTGCAAAACGGGGAAGTCCATCGGATCAGCTGGAAGAAC
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US-09-996-634-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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SEQ ID NO 39
LENGTH: 841
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APPLICANT: Nano, Francis
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-26
CURRENT FILING DATE: 2001-17-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/09996634 Patent No. US20020172684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
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PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/90,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
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NAME/KEY: misc_feature
LOCATION: (1)..(841)
OTHER INFORMATION: n is a,
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147 TrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIle 164
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                                                                    AsnGlyArg----
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                      US-10-008-355-2_COPY_522_712 (1-191) x US-09-815-242-7701 (1-1026)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
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Percent Similarity:
Best Local Similarity:
Query Match:
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Sequence 1729, Application US/09974300; Patent No. US20020146721A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Clausen, ID Groth TITLE OF INVENTION: Methods for Monitoring Multiple TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: 60/279,526
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346 GACCGTTATCGCCAGAAATCCCGATAAGTATGAGTGGTGGAACCTGATTACGATCAACAA 405
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                               56 -SerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLy 75
                                                                                                 36 MetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nArgThrIleSerValAspIleArgTyr-----ValLeuPheMetIleAspLysTr 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGl 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGCACCTGCTGGCGGCCGATGCTGGAAGAGCAGCCACCGCGGTTCCCCGTTCGTCGCCTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pGlyGlnCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u-----AlaMetSerGlyAspIleGluPheGluProAspLeuGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GAAGCCTTCGACAAGACCGCCAAGCTGATCGGCCTGGGCTATCCCGGTGGTCCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rGly-----LysGlyValLeuGluLysGlnAspProLysSerAspGluPheAla--
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Bacillus US-09-974-300-1841
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LENGTH: 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version
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No.:
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                                                                   436 AATAAAGGAAAGGTGATCATCACAAACCCTTATAAAACAGCGTCAACCGGAACGATGGTC 495
                                                                                                                                                                                                                                                                                271 AACGCATCACTCGTAGAAAGACTCGAGCAG-----TACGCCAAGCTGAATCAGGATGTG
                                      77
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ATTACGATTGCGAAGCAGACGGACGGCTCAGGAGTTGTTGCCGTCAACATGAAAATC 555
                                                                                                         GlyLysGly--
                                                                                                                                        GAAGCGATCTACACAGGT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLe 112
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                                  -----ValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIle 94
                                                                                                                                                                        TyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThr 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uHisIleAlaPheLeuSerAsnAsnAspIleThr-----GlyGlyAsnSerGlySe 129
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    LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGl

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APPLICANI: SWARSTOM, RONALD
TITLE OF INVENTION: ALPHAVIRUS VECTORS AND V
TITLE OF INVENTION: VACCINES
FILE REFERENCE: 01113.0001U3
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
LENGTH: 1026
TYPE: DNA
TYPE: DNA
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Best Local Similarity:
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; LOCATION: (1)...(1026)
US-09-991-258-9
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US-09-991-258-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                           No..
451 ATGCATGTGGAAGGCAAGATCGACAACGACGTTCTGGCCGCGCTTAAGACGAAGAAAGCA 510
                                                                           391
                                                                                                                                                334 CCAGGCAAGAGACAGCGCATGGTCATGAAATTGGAATCTGACAAGACGTTCCCAATC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 GATGAGCTTATCAAAGCGACAGAGCGCGTCAACATCGGAAAAAGCGGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 CAATATACATTTGAAGGAAAAGAAAAGAAAATGGCT 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ---LeuAlaPheAspGlyAsnTrpGluAlaMetSer 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 LeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIle 114
                                      70
                                                                                                                                                                                 38 ProGlyArg-----
                                    TyrHisThrThrGlyLys----
                                                                       ATGTTGGAAGGGAAGATAAACGGCTACGCTTGTGTGTCGGAGGGAAGTTATTCAGGCCG 450
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                                                                                                           MetSerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAla-----TrpTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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Johnston, Robert
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Caley, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Davis, Nancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description of Artificial
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                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
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Indels:
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                                  -GlyValLeuGluLysGlnAsp 82
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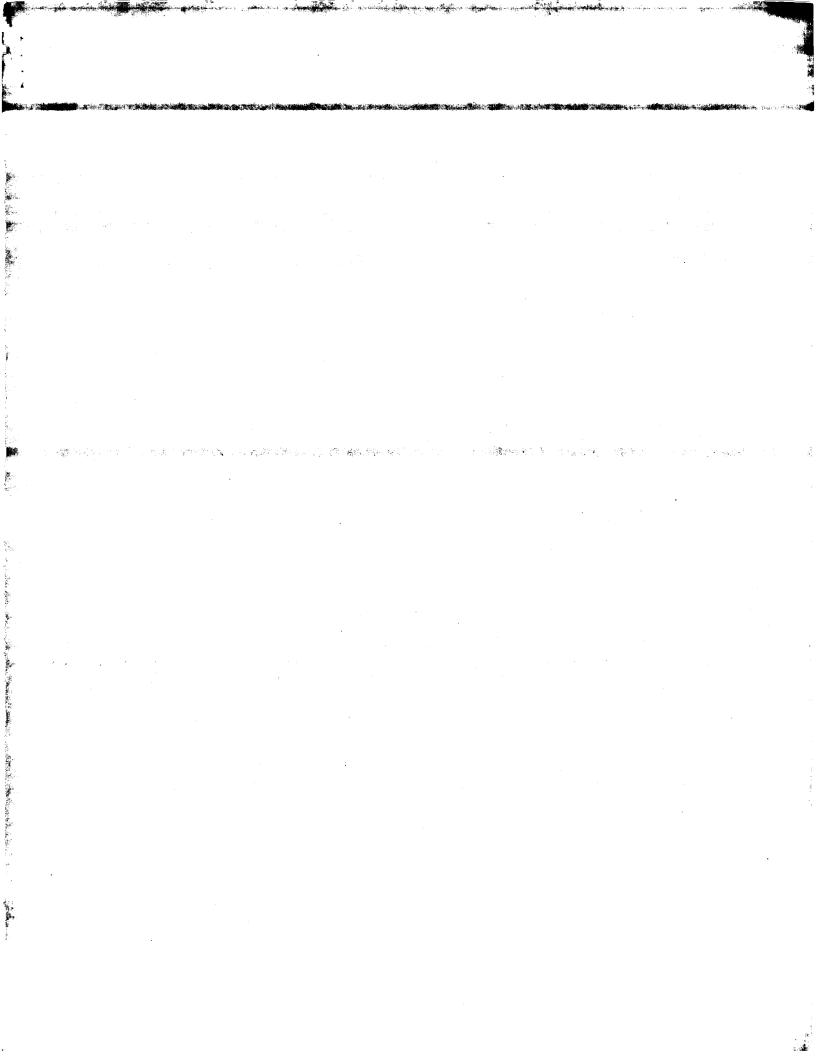
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                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/216,995 PRIOR FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE TITLE OF INVENTION: VACCINES
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 01113.0001U3
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                                                                  --AlaLeuProSerAspAlaAsnPheThrMetArg 51
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Conservative:
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                                                                                                                                                                               Query
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/661,887
PRIOR FILING DATE: 2000-09-14
NUMBER OF CENTRAL PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Styrkarsdottir, Unnur
APPLICANT: Johannsdottir, Vala Drofn
TITLE OF INVENTION: Human Osteoporosis Gene
FILE REFERENCE: 2345.2009-001
CURRENT APPLICATION NUMBER: US/09/952,360
CURRENT FILING DATE: 2001-09-13
                                                                                                                                                                                                                                                                                                                         LOCATION: (3639)...(3984)
NAME/KEY: CDS
LOCATION: (11757)...(12601)
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LOCATION: (36:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                   1377 ACTCCGGAG 1385
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               -----LysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArg 40
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${\tt aAsnPheThrMetArgMetSerTyrGlySerIle}$] V [74-3	vativ	GCGCCGTGGCGCGCGCCTCGCGGCTTTTAAAGGGGACGCCGCCTCCCCGCGCALLLysGlyTyr CCGCGGCGCAACACCTCCCCTTCGCGCGCGCTGCCGGCGCGCACCGCGCGCG
erT	TGA:	euA	00-	·· ve:	GCCGCCTGCCGGCTC :: :: CCGG-GGATCCCCGA hrGlyLysGlyValL :: GCCGCGGCGGGGGTGG snIleLeuAspLeuS
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451 TCCTATATCGTCGGTGCCGGACGGGGCCGGAAGTACCATCCGCAAGCAGGCGCGCATCGCT 510
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511 TTTTCCGGAACTGATGCGAATATCACCGCAATGCTTGGTGATGTGTCGCTTGAA 564
                                                                                                                                                                                                                                                                 304 TACGAAACTGAGAAGGTGCTTGAGGAACACGCGAGGAATCTCGGTGTCTGCATCCTTCGC 363
                           140 GlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGlu 157
                                                                                                                                                                                                                                                                                                                                                                                                                                              259 TCTGCGCTTGACACGCGAGCCAATTTTACACTG------TTCATCCCCCAG 303
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Search completed: December 21, 2002, 11:21:05
Job time: 71 secs



GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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seq
       A_Geneseq_101002:*

1: /SIDSZ/gcgdata/g

2: /SIDSZ/gcgdata/g

4: /SIDSZ/gcgdata/g

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1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs; 133250620 residues
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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and is derived Pred. No. is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

Result No.		Query Match Length DB	Length	DB	ID	Description
ם	1003	100.0	- 7	23	AAO15205	Porphyromonas q
2	274	27.3		23	AA015206	Porphyromonas ging
ω	90	9.0		17	AAR88649	Neisseria menin
4	89.5	8.9		22	AAB95249	Human protein s
ъ	89.5	8.9		22	AAB94310	Human protein segu
σ	89.5	8.9		22	AAM40262	Human polypepti
7	89.5	8.9		22	AAM4 204 8	Human polypepti
8	89.5	8.9	3421	22	AAB84902	Chimeric protein 1
9	86	8.6		23	ABB53805	Lactococcus lacti
10	85.5	œ		<u>ي</u>	220022	プラン・カー・カー・カー・カー・カー・カー・カー・カー・カー・カー・カー・カー・カー・

Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal

of

5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	
77	77	77.5	78	78	78	78	78	78	78	78	78	78.5	79	79.5	80	80	80	80	80	80.5	80.5	80.5	80.5	81	81	81.5	81.5	81.5	82	83	83	84	85.5	85.5	
7.7																					8.0												8 . 5		
332	180	971	3432	870	846	803	781	684	509	215	52	498	571	389	392	357	344	344	336	4643	1317	532	532	283	283	309	254	240	870	360	201	537	323	321	
21	23	19	21	22	21	21	21	22	22	17	23	21	18	23	17	L U	8	17	13	22	22	18	17	23	21	23	22	22	21	23	22	18	21	21	
AAY68962	AAU75485	AAW48896	ABB07037	AAB94408	AAG31211	AAG31212	AAG31213	AAM93433	AAM25688	AAR91044	AA015207	AAY75500	AAW16399	ABB53562	AAR91034	AAR26842	AAW22218	AAR91033	AAR29644	ABB71609	ABG18723	AAW22219	AAR91035	AAU96101	AAY71478	ABP25673	AAU36684	AAU33855	AAB41742	ABP39512	AAG82591	AAW22220	AAG40031	AAG40032	
Cps2J protein whic	s antigen	Candida albicans C	Japanese encephali	۳.		Arabidopsis thalia	Arabidopsis thalia	Human polypeptide,	Human protein sequ	V8 mature protease	Staphylococcus aur	Neisseria meningit	Konjak mosaic viru	Lactococcus lactis	OI	Protease from S. A	Protein encoded by	Beta-galactosidase	Protease from S. A	Drosophila melanog	Novel human diagno	Protein encoded by	ĸ,	Ehrlichia canis p2	Ehrlichia canis im	77		Staphylococcus aur	Human ORFX ORF1506	taphylococcus	 S. epidermidis ope 	0	thali	Arabidopsis thalia	

ALIGNMENTS

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RESULT 1
AAO15205
                                                                                                                                                                                                  Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis;
                         WPI; 2002-490075/52.
N-PSDB; AAL43635.
                                                     Travis J, Potempa JS,
                                                                                          08-NOV-2000; 2000US-246827P
                                                                                                               08-NOV-2001; 2001WO-US46782
                                                                                                                                  16-MAY-2002.
                                                                                                                                                                                            periodontitis.
                                                                                                                                                                                                                                                     05-SEP-2002
                                                                                                                                                                                                                                                                         AAO15205;
                                                                                                                                                                                                                                                                                           AA015205 standard; Protein; 712 AA
                                                                                                                                                     WO200238742-A2.
                                                                                                                                                                        Porphyromonas gingivalis.
                                                                                                                                                                                                                                Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7).
                                                                        (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                   (first entry)
                                                      Banbula A,
                                                      Bugno M;
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RESULT 2
AAO15206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the
Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal
                                             WPI; 2002-490075/52.
                                                                                                                            08-NOV-2000; 2000US-246827P
                                                                                                                                                       08-NOV-2001; 2001WO-US46782
                                                                                                                                                                                                            WO200238742-A2
                                                                                                                                                                                                                                    Porphyromonas gingivalis
                                                                                                                                                                                                                                                                 periodontitis.
                                                                                                                                                                                                                                                                            Dipeptidylpeptidase-7; DPP-7; er DPP-7 inhibitor identification;
                                                                                                                                                                                                                                                                                                                   Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) C-terminal region
                                                                                                                                                                                                                                                                                                                                              05-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                         AA015206;
                                                                                                                                                                                                                                                                                                                                                                                                    AAO15206 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylepetidase-7 (PPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease caused by Porphyromonas gingivalis
                                                                                                                                                                                 16-MAY-2002
                                                                                                 (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SKSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPRLIQELKLI 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPRLIQELKLI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGY 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 4; 65pp;
                                                                      Potempa JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                      DPP-7; enzyme;
                                                                      Banbula
                                                                                                                                                                                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1003; DB 23; Pred. No. 9.6e~101;
                                                                                                                                                                                                                                                                                                                                                                                                    À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                      Ą
                                                                                                                                                                                                                                                                            periodontal disease;
                                                                      Bugno M;
                                                                                                                                                                                                                                                                                          amidolytic cleavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                            gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 3
AAR88649
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
           Jacobs E,
Millet MBJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontifis). The present amino acid sequence represents the c-terminal region of the Porphyromonas gingivalis dipeptidylpeptidase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptid/slpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.
                                                                                           31-MAY-1994;
                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferrin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis BZ163 transferrin receptor Tbp2 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR88649 standard; Protein; 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease caused by Porphyromonas gingivalis
                                               (INMR ) PASTEUR ME
(TRGE ) TRANSGENE
                                                                                                                     30-MAY-1995;
                                                                                                                                                07-DEC-1995
                                                                                                                                                                           WO9533049-A2
                                                                                                                                                                                                                                Doma in
                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   passive immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR88649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DPP-7) enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
52; Conserv
                                                               PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis (strain BZ163).
                       Legrain M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                     95WO-FR00701.
                                                                                           94FR-0006594.
                                                                                                                                                                                                                                                                    /note= "N-terminal domain" 367..564
                                                                                                                                                                                                                                        /label= Domain_2
/note= "hinge domain"
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                     /note= "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                   /label= Tbp2_subunit
                                                                                                                                                                                                                   'label-
                                                                                                                                                                                                                                                                                                                       'label signal_peptide
                                                   SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tbp2 subunit; deletion mutant; vaccine
                         Mazarin V,
                                                                                                                                                                                                                   Domain_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 274; DB 23;
Pred. No. 1.7e-22;
                                                                & VACCINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   IM2169; IM2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 4
AAB95249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
  PTT PTT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domains (see features table); deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. The positions of the 3 domains in BZ163 are defined by alignment with the IMZ169 sequence. The deletion mutant polypeptides of the invention can generate an immune response against N.meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT11244
                                                                                                                                       27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767
                                                                                                                                                                                                                                                                                                       Human; primer;
                                                                                                                                                                                                                                                                                                                               Human protein sequence SEQ ID NO:17413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 82-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tbp2
              Primer sets
                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                               07-FEB-2001
                                                                                                                                                                                                                                                        EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                   AAB95249;
                                                                                                                                                                                                                                                                                                                                                                                                            AAB95249 standard;
 Primer sets for synthesizing full-length cDNAs defined in
                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                              09-JUN-2000;
                                                                                                                                                                                                      28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                          26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transferrin Tbp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNNDITGGNSGSPVFDKIGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV
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                                                                ß
                                                             Isogai T,
Sugiyama
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                                                                                                                            2000JP-0241899
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                                                                                                                                                                             99JP-0248036
                                                                                                                                                                                                                                                                                                      detection; diagnosis; antisense therapy; gene therapy
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                                                               Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.0%;
                                                                hikawa T,
Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the N.meningitidis strain BZ163 e Tbp2 polypeptide has three
polynucleotides, particularly the 5602 the specification, and for the detection
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                                                               Hayashi K,
A, Nagai K,
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1.2;
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                                                                            Saito
                                                                aito K,
Otsuki
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                                                                Η,
                                                                            Yamamoto
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29-JUL-1999; 27-AUG-1999; 11-JAN-2000; 02-MAY-2000; 09-JUN-2000;

2000JP-0118776. 2000JP-0183767. 2000JP-0241899.

28-JUL-2000; 07-FEB-2001

2000EP-0116126

99JP-0248036.

99JP-0300253

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RESULT 5
AAB94310
ID AAB9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; aAB92446 to AAB95893 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                            EP1074617-A2
                                                                                                                                                                                                                                                                                                             26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                            AAB94310 standard;
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                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                           Human; primer;
                                                                                                                                                                                                                                                                             Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM----SYGSIKGYEPQDGAWYNYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGNDVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY
                                                                                                                                                                                                                                                                         protein sequence SEQ ID NO:14779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                         detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                          entry)
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Pred. No. 1
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                                                                                                                                                                                                                                       gene therapy
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RESULT 6
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Best Local S
Matches 42
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                                      chemokinetic;
                                                    peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy;
peripheral nervous system; neuropathy; central nervous system;
                                                                                                                                                 Human polypeptide SEQ ID NO 3407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence and an oligonucleotide comprising a sequence complementary to polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                ieukaemia
                                                                                                                                                                                                                                                                       AAM40262 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 14779; 2537pp +
                                                                                                                                                                                            22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYGVRRGRYCFEMKINEEISVKHLPSTEPDPHYVRIGWSLDSCSTQLGEEPFS---YGYG 305
                                                                                                                                                                                                                                                                                                                                                                    CGNDVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM----SYGSIKGYEPQDGAWYNYH 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                          (first
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T, Wakamatsu A,
                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 89.5;
25.1%; Pred. No. 1
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                                  drug
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 856;
                                                                                                                                                                                                                                                                                                                                                                      383
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RESULT 7
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Best Local S
Matches 42
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
Wang
                                                                                                                                                                                                                                                                                                                                                Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
AAM42048 standard; Protein;
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                           C.N.S disorders
Note: The sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                               specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such as
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19-OCT-2000;
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                                                                                             125
                                                                                                                        306
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                                                                                                                                                 72
                                                                                                                                                                                                    19
                                                                                                                                                                                                                              Local Similarity les 42; Conser
                                                                                                                        GTGK--
                                                                                                                                                                          SYGVRRGRYCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS---YGYG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QA,
                                                                   CGNDVELSFTKNGKWMGTAFRIQKEALGGQALYPHVLVKNCAVEFNF
                                                                                                                                               TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG-----
                                                                                                                                                                                                    AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM----SYGSIKGYEPQDGAWYNYH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-442253/47.
                                                                                          -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang 2
Zhou
                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                    866 AA;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u C,
u P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO 3407; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                           data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodrich
                                                                                                                                                                                                                                         8.9%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                          for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system injuries
                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŗ
                                                                                                                                                                                                                            Score 89.5; DI
Pred. No. 1.8;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen R,
Xu C,
                                                                                                                        -SRFENYGDKFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ma Y,
Xue AJ,
? RT;
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8
                                                                                                                                                                                                                                                          DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qian XB,
Yang Y,
                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                       Length
                                                                                                                        NDVIGCEADEE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F,
                                                                                                                                                                                                                                                           866;
                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                               Gaps
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AAM42048

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                                                                                                                                Query Match
Best Local
                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
Wang
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 6979; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-2000;
19-JUL-2000;
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25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human: nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-2001
                                                                                                                                                                                                       specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia.
 363
                                                         306
                      72 TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG----- 124
                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          у J,
QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-442253/47.
 GTGK----
                                                      SYGVRRGRYCFEMKINEEISYKHLPSTEPDPHYVRIGWSLDSCSTQLGEEPFS---YGYG 362
                                                                                   AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
                                                                                                                                                                                                                   The sequence data for this patent did not
                                                                                                                  l Similarity
42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI61204
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Wang Z,
Zhou P,
                                                                                                                                                                          923 AA;
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2000US-0552317.
2000US-0558042.
2000US-0650312.
2000US-06530312.
2000US-0662191.
2000US-06631036.
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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 -KSTN----
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodrich
                                                                                                                                8.9%;
25.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides, useful for treating disorders
system injuries -
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                                                                                                                  22;
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 ----SRFENYGDKFAE-----
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, Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6979
                                                                                                                Pred. No. 2;
2; Mismatches
                                                                                                                              Score 89.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hen R, Ma Y, (
Xu C, Xue AJ,
Drmanac RT;
                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qian XB,
. Yang Y,
                                                                                                                                            22;
                                                                                                                56;
                                                                                                                                                                                                                form
                                                                                                                                          Length 923;
                                                                                                                Indels
                                                                                                                                                                                                                  part
NDVIGCFADFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, V
Zhang J;
                                                                                                                47;
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                                                                                                             Gaps
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RESULT 8
AAB84902
ID AAB8
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PA
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                                                                                                                     Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                   The invention relates to a chimeric live, infectious, attenuated virus comprising a yellow fever virus with the nucleotide sequence encoding a prM-E protein deleted, truncated or mutated so that functional yellow fever virus prM-E protein is not expressed and also integrated into the genome of the yellow fever virus a nucleotide sequence encoding a prM-E protein of a second, different flavivirus so that the prM-E protein of the second flavivirus is expressed. The chimeric live, infectious, attenuated virus is used to prepare medicaments for preventing or treating flavivirus infection in a patient. The yellow fever virus vector produces its gene product (tumor antigen or cytokine) in cells of the lymphoid or reticuloendothelial system or in a precursor of these systems in patients with cancer. Flaviviruses replicate in the cytoplasm of cells so that the virus replication does not involve integration of the viral genome into the host cell. The present sequence represents a chimeric
                                                   1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric live, infectious, attenuated yellow fever viruses used for preventing and treating diseases caused by flaviviruses have prM-E nucleotide sequence from a second, different flavivirus as functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chambers TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavivirus febricis.
Japanese encephalitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; virucide; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric protein from yellow fever virus and Japanese encephalitis virus
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                    protein derived from yelllow fever virus and Japanese encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 200-215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yellow fever prM-E is not expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-343953/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2000; 2000WO-US32821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200139802-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yellow fever virus; prM-E protein; flavivirus; chimeric; medicamen infection; tumor antigen; cytokine; lymphoid; reticuloendothelial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
                                                                                     19
                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGNDVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
-TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
                                                 AFLVRNGKKL----
                                                                                   AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY 170
                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF83821
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                        3421 AA;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0452638
                                                                                                                                   8.9%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΤP,
                                                 -----IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guirakhoo
                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3421 AA
                                                                                                                                     Score 89.5;
Pred. No. 14;
                                                                                                                     Mismatches
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                                                                                                                                                      DΒ
                                                                                                                     46;
                                                                                                                                                      22;
                                                                                                                                                     Length 3421;
                                                                                                                     Indels
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RESULT 9
 В
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                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                      production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent W0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                            The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1596
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                              New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis protein dnaE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB53805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB53805 standard; Protein; 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-2002
                                                                                                                                                                                                                                                                                   invention helps research in lactic bacteria, particularly useful in the
                      154
                                           850
                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131
                                                                                     790
                                                                                                                                743
                                                                                                                                            14 DAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFT----MRMSYGSIKGYEPQDGAWYN 69
                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1665
                    IEFEPDLQRTISVDIRYVLFMIDKWGQ 180
                                                                DITGGNSGSPV-
                                                                                    ENQPYKDLADFVEKLPNNFHKKENILPLIQIGAFDYADSNRGKLAYNLADHANLLNYYSD
                                                                                                                                DALENGFEIEK - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVPGKNVVNVQTKPS------LFKVRNGG---EIGAVAL-----DYPSGTSGSP 1635
                                         DIFMASSGGGFAYHEAEDYSETEKYDFEKN--LLGIGVTPHPLQNLARRFEGNFTPLA-- 905
                                                                                                        YHTTGKGVLEKQDPKSDEFAVQENILDL-----FRTKNYGRYAENGQLHIAFLS--NN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
-QLVKNRRMTILVEINYIRTHRTKTGQ 931
                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 507; 2504pp; French.
                                                                                                                                                                                                                     1060 AA;
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                     8.6%;
21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renault P,
                                                                                                                                                                         31;
                                                                                                                                                                        Score 86; DB Pred. No. 6; 31; Mismatches
                                                               ----FDKNGRLIGLA------
                                                                                                                              PSINLMKIGDFVKNKKIRLGLAHVQGISRDLAKWIV 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrlich SD
                                                                                                                                                                                               23;
                                                                                                                                                                         73;
                                                                                                                                                                                             Length 1060;
                                                                                                                                                                         Indels
                                                               -- FDGNWEAMSGD 153
                                                                                                                                                                         58;
                                                                                                                                                                        Gaps
                                                                                    849
                                                                                                                                                                                                                                                                                                                               of
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RESULT 10
AAG40033
                                                                                04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
                                                                                                                                                                                                                                                                        06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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NWEAMSGDIEFEPDLQRTISVD--IRYVLFMI 175

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В
                     The invention relates to new mutant Staphylococcus aureus V8 proteases CC which have enzyme activity even under environmental conditions which protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino caids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 53 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the V8 protease fragment; is a second R6 linker and a fragment of the caminoglucoside 3'-phosphotransferase protein. The chimaeric sequence was generated by restriction digestion and ligation from the V8RPT(-) CC sequence (see AAW22218) by using a natural EcoRV site which removed a CC further 8 amino acid from the C-terminus. This truncated V8 protease, CC designated V8F, retains its level of activity in the presence of a cc NXXXX
                                                                                                                                                                                                                                                                                                          Claim 8; Page 19-20; 42pp; English
                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus V8 protease mutants - with increased
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                                                                                                                                                                                                                                                                                                                                           denaturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95JP-0170086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125..339
/note= "truncated S. aureus V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..100
/note= "E. coli beta-galactosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "R6 linker sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "R6 linker sequence"
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                                                                                                                                       of
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Sequence

Query Match Best Local Similarity

8.3%; 24.5%;

Score Pred.

No.

DB 1.1; 22;

Length 201;

Sequence

201 AA;

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RESULT 14
AAG82591
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                                                                                                                                                                                                                                                                                                                                                                                                                              DR DR PT PT
                                                                                                          CC (II), given in AAG81454 to AAG83120, from Staphylcoccous epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC s. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CN.B. The present invention of the present invention.
CC N.B. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding useful for vaccinating
                                              N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                        AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 606; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kimmerly WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. epidermidis open reading frame protein sequence SEQ ID NO:2276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG82591 standard; Protein;
                               no sequences are present for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RWGR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWGQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFELRLYRRHH 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0164258
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28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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Pred No. 3.6;
                               SEQ ID
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                                 NO:4455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                             to 4464.
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RESULT 15
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                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID 4357; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-1997;
08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 -----IEFRGFSQKTV 126
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20
                                                                                      57 IKGYEPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRT-KNY-----GRYAEN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
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                                                                                                                                                                                                                                              Local Similarity
MKGAHPMKNIKKPFDLKGKSLLKEYDLTGEEF - - - EGLIDFAMTLKKYKQQGTPHRYLEG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQL-----HIAFLSNNDITGGNSGSPVFDKNGRLIGLAFDG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNIALLFEKTSTRTRAAFTVASIDLGAHPEFLGKNDIQLGKKES--VEDTAKVLGRMFDG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKGAHPMKNIKKPFDLKGKSLLKEYDLTGEEF - - - EGLIDFAMTLKKYKQQGTPHRYLEG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site
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                                                                                                                                                                                           Conservative
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97US-064964P.
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                                                                                                                                                                                                                                    8.3%;
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                                                                                                                                                                                      Score 83; DB 23;
Pred. No. 2.6;
15; Mismatches 46
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----IEFRGFSQKTV 145
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Search completed: December 20, Job time: 79 secs 2002, 17:18:58

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OM protein - protein search, using sw model
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// cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
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US-10-008-355-4
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Sequence 2, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 1351, App
Sequence 12777, A
Sequence 4, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 6, Appli
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6.6	6.6	6.7	6.7	6.7	6.7	6.7	6.7	6.7		6.7					•	•		6.9		7.0		٠		7.2	7.2
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US-09-925-297-718	6-468-2	5-242-11	US-09-815-242-13866	9-964-	US-10-062-624-9	US-09-846-808-19	-062-9	US-10-062-994-18	5-299-9	5-2	US-09-815-242-5859	US-10-095-139-8	US-09-344-882-16		-094	-299-	US-09-815-242-10274	US-09-815-242-11798	-781-	5-24	US-10-135-322-10	-300 - 1	US-10-059-964-40	US-09-987-107-46	US-10-062-994-4
e 718,	Sequence 21, Appl			,2	9	19,	18,	18,	Ø	12894,	Sequence 5859, Ap	<i>3</i> , 8		62,	2, Appl	911	Sequence 10274, A			e 13511	10,	Ø	e 40,	46,	Sequence 4, Appli

ALIGNMENTS

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US-10-008-355-2
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Patent No. US30020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potenpa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And
FILE REFERENCE: 235.004440101
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 191; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 712
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
702
                                  181 CPRLIQELKLI 191
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                                                                  DITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMIDKWGQ 180
CPRLIQELKLI 712
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Pred. No. 3.7e-96;
); Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Aggieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Mei
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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; LENGTH: 720
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-008-355-9
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US-10-008-355-9
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TYPE: PRT
CORGANIZM: Porphyromonas gingivalis
US-10-008-355-8
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
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                                                                                                                                                                                    Query Match 42.6%; Score 427.5; DB 9; Best Local Similarity 47.4%; Pred. No. 1.9e-36; Matches 81; Conservative 34; Mismatches 55;
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APPLICANT: Potempa, Jan S
APPLICANT: Benbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
TITLE REFERENCE: 235 00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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                                          82 DPKSDEFAVQENILDLFRTKNYGRYAE-NGQLHIAFLSNNDITGGNSGSPVFDKNGRLIG 140
                                                                                                                                          22 IEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYEPQDGAWYNYHTTGKGVLEKQ 81
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DPDNWEFVVDPKLKAVYERKDFGRYADRSGRMPVAFCATTHTTGGNSGSPVMNANGELIG
                                                                                           ILRAQRTYIAGLLEMDGDQDQFPDANLTLRFTYGQVKGYSPRDNYYYGHQTTLDGVMEKE 608
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; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-008-355-7
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                                                                                                       ; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
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Best Local Similarity
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Patent No. US20020164759A1
Best Local Similarity
                     Query Match
                                                                                                                                                                                    APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER: OF SEQ. ID NOS: 26
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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APPLICANT: Banbula, Agniesźka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
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                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
                                                                               ORGANISM: Porphyromonas gingivalis
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27.3%;
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Score 274; DB 9;
Pred. No. 5.1e-22;
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Pred. No. 9.5e-27;
0; Mismatches 53
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                                           ; ORGANISM: Shewanella putrefaciens US-10-008-355-5
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                                                                                                  SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 734
                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10008355 Patent No. US20020164759A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 67; Conserv
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LENGTH: 732
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    Query Match
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APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
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APPLICANT: Banbula, Agnisszka
APPLICANT: Banbula, Agnisszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/246,827 PRIOR FILING DATE: 2000-11-08
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                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                688 AITKDWFFNPTITRAVHVDIRYILWMMDEVDHADNLIKELDLV 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMSGDIEFEPDLORTISVDIRYVLFMIDKWGQCPRLIQELKLI 191
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  25.5%;
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  Score 255.5;
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                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Staphylococcus aureus US-09-815-242-5351
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LENGTH: 240
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                                                                                                                                                                                                                                        Matches
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Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION NUMBER: 60/206,848
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213 VKNDDNRNAYG--VYFTPEIKKFIAENI 238
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                                     ---DGNWEAMSGDIEFEPDLQRTISVDI
                                                                                                               QENILDLFRTKN----YGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGLAF--- 143
                                                                                                                                                      YPGKEDVSVIQVEERAIERGPKGFNFNDNVTPFKYAAGAKAGDRIKVIGYPHPYKNKYVL 167
                                                                                                                                                                                             YPGRALPSDANFTMRMSYGSIKGYEPQDGAW-YNYHTTGKG-----VLEKQDPKSDEFAV 90
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                                                                            HESTGPVMSVEGSSIVYSAHTES ---
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                                                                                                                                                                                                                                  8.1%; Score 81.5; DB 23.0%; Pred. No. 0.36; tive 22; Mismatches
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                                     168
                                                                              --GNSGSPVLNSNNELIGIHFASD 212
                                                                                                                                                                                                                                                                           DB 10;
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                                                                                                                                                                                                                                                                         Length 240;
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RESULT 10
US-10-062-624-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus aureus US-09-815-242-12277
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                                                                                            GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D61520172/D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12277
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                              Sequence 4, Application US/10062624 Patent No. US20020115840A1
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                   PRIOR APPLICATION NUMBER: 09/660,587 PRIOR FILING DATE: 2000-09-12
                                                           CURRENT APPLICATION NUMBER: US/10/062,624
CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, APPLICANT: Ohlsen, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in
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  NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                           144 --- DGNWEAMSGDIEFEPDLQRTISVDI 168
                                                                                                                                                                                                                                                                                                                                                                     227 VKNDDNRNAYG--VYFTPEIKKFIAENI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 QENILDLFRTKN----YGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGLAF--- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 YPGRALPSDANFTMRMSYGSIKGYEPODGAW-YNYHTTGKG-----VLEKODPKSDEFAV 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HESTGPVMSVEGSSIVYSAHTES-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPGKEDVSVIQVEERAIERGPKGFNFNDNVTPFKYAAGAKAGDRIKVIGYPHPYKNKYVL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
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ID NOS: 46
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23.0%;
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Pred. No. 0.38
22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
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; FEATURE:
; OTHER INFORMATION: amino acid sequence of p28-5 protein
US-10-062-624-4
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US-10-008-355-4
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 283
                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Sequence 21, Application US/09767041 Patent No. US20020055168A1
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Best Local Similarity
Matches 16; Conserv
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Best Local
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                                                                                                 CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/0046
PRIOR FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
                                                                                                                                                                                                    APPLICANT: Smith, I
                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                           PRIOR APPLICATION NUMBER: EPS PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                   FILE REFERENCE:
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                              123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 VYLINEGLLNISFMTNICYETASKNIPLSPYICAGIGTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 VFDKNGRLIGLAFDGN--WEAMSGDIEFEPDLQRTISVDI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 SPRIE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 KGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP---- 130
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                                                                                                                                                                                                                                                                                                                                                                                        1 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHF 51
                                                                                                                                                                                                                           Smith, Hilda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                       1998-07-22
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                                          EP98202467.1
                                                                              EP98202465.5
                                                                                                                      PCT/NL99/00460
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Pred. No. 0.11
13; Mismatches
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Pred. No. 0.5;
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NAME/KEY: misc_feature
; OTHER INFORMATION: CPS2U
US-09-767-041-21
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SEQ ID NO 21
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                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
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                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975Ale OTHER INFORMATION: synthetic construct -09-991-258-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/216,995
PRIOR FILING DATE: 2000-07-07
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                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 34
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 01113.0001U3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE TITLE OF INVENTION: VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptococcus
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                                      171 SKYDLEYADVPQNMRADTFKYTHEKPQGYYSWHHGAVQYENGRFTV---PKGVGAKGDSG 227
                                                                                                                      112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 SNNDITGGNSGSPVF------DKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIR 169
                                                                           83 PKSD-EFA-VQENI-LDLFR---TKNYGRYA-----ENGQLHIAFLSNNDITGGNSG 128
                                                                                                                                                       38 PGR-----ALPSDANFTMRMSYGSIKGYEPQDGA--WYNYHTTGK-----GVLEKQD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 DSDDIVDGNIVESLYTCLKENDSDLSGGLLA-TFDGNYQ------ESELQK-CQIDLE 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 7.7%;
Local Similarity 25.4%;
                                                                                                                                                                                                                   Local Similarity 24.5%;
                                                                                                                PGKRORMVMKLESDKTFPI-MLEGKINGYACVVGGKLFRPMHVEGKIDNDVLAALKTKKA 170
SPVFDKNGRLIGLAFDG------NWEAMSGDIEFEPD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THLEILLIDDGSSDSSTDICLEYAEQDGRIKLFRLPHGGVSNARNYG-IKNSTANYIMFV 88
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o. US20020141975A1
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24.5%; Pred. No. 3;
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 44
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11154, Applicatio Patent No. US20020061569A1
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Best Local :
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                                                                                          APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, SOJEN
TITLE OF INVENTION: APPLIFOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
                PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-33
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: pT7 H6Ubifx Apo A-1 plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 SVTSTFSKLREQLGPVTQEFWDNLEKETE---GLRQEMSKDLEEV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 SGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 KRLFFAGLREMYPGRALPSDAN------FTMRMSYGSIKGY---EPQDGAWYNYHTTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336
                                                                                                                                                                                                                                                                                      Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                        Carr, Grant J.
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Pred. No.
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Gaps

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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11154
LENGTH: 436
TYPE: PRT
ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(436)
OTHER INFORMATION: Xaa - Any Amino Acid
US-09-815-242-11154
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Search completed: December 21, 2002, 01:47:39 Job time : 24 secs
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                                                                                      · 136 ELNGTA 141
                                                                                                                                137 RLIGLA 142
                                                                                                                                                                          77 QAIVGKDATNQAEIDQIMIDLDGTENKSNFGANAILAVS-LANAKAAAASKGLPLYAYIA 135
                                                                                                                                                                                                 31 FVGL-----AAAPSGA-----STGSREALELRDGDKSRF--LGKGVLKAVAAVNNEIA 76
                                                                                                                                                                                                                                                                                          30 FAGIREMYPGRALPSDANFTMRMSYGSIKGYEPQDGAWYNYHTTGKGYLEKQDPKSDEFA 89
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Result
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
2: /ggn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
      SKSVIAAARAIQADAMANAY......LFMIDKWGQCPRLIQELKLI 191
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/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-134-001C-4357
US-08-941-357-3
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US-08-968-63-3
US-09-960-587-4
US-09-261-358A-4
US-09-261-358A-4
US-09-261-358A-4
US-08-657-192-9
US-08-657-192-3
US-08-533-373-5
US-08-533-373-24
US-08-523-373-24
US-08-523-373-23
US-08-523-373-23
US-08-523-373-24
US-08-9135-166-10
US-08-9135-166-10
US-08-9135-166-10
US-08-926-942-53
US-08-93-326-4
US-08-93-326-4
US-08-93-326-4
US-08-93-326-4
US-08-93-326-7
US-08-068-17-4
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457, Appl 437, Appli 3, Appli 3, Appli 3, Appli 4, Appli 4, Appli 5, Appli 6, Appli
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123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMI-----D 176

1;

Query Match 8.4%; Best Local Similarity 28.1%; Matches 18; Conservative 16	US-08-657-192-15 US-08-657-192-15 Sequence 15, Application US/08657; Patent No. 5747321 GENERAL INFORMATION: APPLICANT: YABUTA, Masayuki APPLICANT: YABUTA, Masayuki APPLICANT: OHSUYE, Kazuhiro ITITLE OF INVENTION: MUTANT ST. TITLE OF INVENTION: PROTEASES NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS: ADDRESSEE: BURNS, DOANE, SW. STREET: P.O. Box 1404 CITY: Alexandria STATE: Virginia COUNTRY: United States IF 22313-1404 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Patentin Release CURRENT APPLICATION NUMBER: US/08/6 FILING DATE: 03-JUN-1996 CLASSIFICATION LOATA: APPLICATION NUMBER: US/08/6 FILING DATE: 02-JUN-1996 CLASSIFICATION NUMBER: 07-17 FILING DATE: 02-JUN-1996 ATTORNEY/ACENT INFORMATION: NAME: Meuth, Donna M. REGISTRATION NUMBER: 36,607 REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-620 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: protein	28 72.5 7.2 691 2 US 29 72.5 7.2 692 3 US 30 72.5 7.2 692 4 US 31 72.5 7.2 711 1 US 32 72.5 7.2 711 2 US 33 72.5 7.2 711 2 US 34 72.5 7.2 711 3 US 35 72.5 7.2 711 3 US 36 72.5 7.2 711 4 US 37 72.5 7.2 711 4 US 38 72.5 7.2 711 4 US 41 72.5 7.2 711 4 US 42 72.5 7.2 72 72 3 US 43 72 72 792 3 US 44 72 72 792 4 US 45 71.5 7.1 369 1 US
Score 84; DB 1; Length 537; pred. No. 0.92; Mismatches 24; Indels 6;	STAPHYLOCOCCUS AUREUS V8 ES SWECKER & MATHIS le MS-DOS e #1.0, Version #1.30 e #1.70086 170086 170086	S-08-449-733-2 Sequence S-08-448-194-62 Sequence S-08-867-921-62 Sequence S-08-478-735-98 Sequence S-08-478-373-98 Sequence S-08-474-671-98 Sequence S-08-478-194-8 Sequence S-08-483-577A-98 Sequence S-08-483-577A-98 Sequence S-08-637-634-98 Sequence S-08-637-654-98 Sequence S-08-637-654-98 Sequence S-08-637-654-98 Sequence S-08-637-654-98 Sequence S-08-637-654-98 Sequence S-08-638-93-166-8 Sequence S-08-135-166-8 Sequence S-08-230-047-5 Sequence S-08-230-047-5 Sequence S-08-230-047-5
Gaps 1		2, Appli 62, Appl 98, Appl 98, Appl 98, Appl 98, Appl 98, Appli 98, Appli 98, Appli 8, Appli 8, Appli 8, Appli 8, Appli 8, Appli 8, Appli 98, Appli 98, Appli 98, Appli 98, Appli

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US-08-491-357-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LYND DOUCETTE-Stamm et al
APPLICANT: LYND DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-8-13
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Applic Patent No. 5716782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4357
LENGTH: 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     APPLICANT: Estojak, JOAnne
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: MEDIATO
TITLE OF INVENTION: ALTERAT
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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  APPLICATION NUMBER:
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 MKGAHPMKNIKKPFDLKGKSLLKEYDLTGEEF --- EGLIDFAMTLKKYKQQGTPHRYLEG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 IKGYEPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRT-KNY-----GRYAEN 109
                                                                                                                                                                                                                        ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KWGQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IEFRGFSQKTV 145
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                                                                                                                                         19103-2307
                                                                                                                                                                                                     Philadelphia
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                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                        Law, Susan
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24.5%;
                                                                                                                                                                                                                                                                                                     NUCLEIC ACID MOLECULE MEDIATOR PROTEIN THAT ALTERATIONS
US/08/491,357
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Pred. No. 0.66;
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                                                                                                                                                                                                                                                                                                                       ENCODING A SIGNAL INDUCES CELLULAR MORPHOLOGICAL
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Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Golemis, Erica A.
APPLICANT: Law, Susan
APPLICANT: Estojak, Joanne
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: MEDIATOR
TITLE OF INVENTION: ALTERATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
DESCISSERATION NUMBER: 36,252
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
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TELEPAX: (215) 563-4044
                                                     ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
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LENGTH: 872 amino acids
                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1601 Market CITY: Philadelphia
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                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/968,633
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
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: (215) 563-41
(215) 563-4044
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                    563-4100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erica A.
                                                                                                                                       US/08/491,357
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Pred. No. 3.1;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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LENGTH:

872 amino acids

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                                                                                                                                      TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: No. 6100384 Relevant
TOPOLOGY: No. 6100384 Relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ESTOJAK, JÓANDE
TITLE OF INVENTION: NÚCLEIC ACID MOLECULE ENCODING A SIGNAL
TITLE OF INVENTION: MÉDIAFOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA;
APPLICATION NUMBER: 08/491,357
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
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HYPOTHETICAL:
                  MOLECULE TYPE:
                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 GNIVRQGK----GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 PSDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDL 97
                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                   STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 8.2%; Score 82; DB Local Similarity 24.3%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                            ENGTH:
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                                                                         amino acid
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1601 Market Street Suite 720
                                                                                            872 amino açids
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              protein
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Best Local Similarity
Matches 43; Conserv
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                                                                        Query Match
Best Local Similarity
                                                             Matches
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                                                                                                                                                                                                                                          TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                      HYPOTHETICAL: ANTI-SENSE:
                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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580 TLVACSRAVPEDAKQLASFLHGNASLLFRRTKAPGPGPEGSSSLHLNPTDKASSIQSRPL 639
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                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
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                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
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01 Market Street Suite 720
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                                                                          8.2%; Score 82; I
24.3%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERATIONS
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Pred. No.
                                                            Mismatches
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                                                             Indels
                               ----RAL 42
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CURRENT APPLICATION NUMBER: US/09/660,587
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 09/261,358
PRIOR FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 4
SEQ ID NO 5: 46
SEQ ID NO 4
SEQ ID NO 5: 46
; OTHER INFORMATION: amino acid sequence of ECa28SA2 protein US-09-261-358A-4
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APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
                                                                     SEQ ID NO 4
LENGTH: 283
TYPE: PRT
ORGANISM: Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09261358A Patent No. 6403780
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APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2
                                                                                                                                                                         FILE REFERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                         APPLICANT: Yu, Xue-Jie TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof FILE REFERENCE: D6152CIP
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                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 VFDKNGRLIGLAFDGN--WEAMSGDIEFEPDLQRTISVDI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 SPRIE-----VEMSYEAFDVKNPGDNYKNGAYRYCALSHQDDADDDMTSATDKF 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 8.1%; Score 81; DB 4; Length 283; Local Similarity 26.9%; Pred. No. 0.77; les 43; Conservative 20; Mismatches 67; Indels
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US-08-657-192-9
                                                                                Query Match
Best Local Similarity
Matches 18; Conserv
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Best Local
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APPLICANT: YABUTA, Masayuki
APPLICANT: OHSUYE, Kazuhiro
                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-170086

FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 001560-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                       123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLF-MIDKWGQ 180
289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDRLYRRHHRWGR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 VYLINEGLLNISFMTNICYETASKNIPLSPYICAGIGTDL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 VFDKNGRLIGLAFDGN--WEAMSGDIEFEPDLQRTISVDI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01
FILING DATE: 03-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watch 8.1%; Score 81; E Local Similarity 26.9%; Pred. No. 0.
                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 EKGKRLFFAGLREMYPGRALPS---DANFTMR---MSYGSIK--GYEPQDGAWYNYHTTG 74
                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 KGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP---- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKKTTVVYGLKENWAGDAISSQSPDDNFTIRNYSFKYASNKFLGFAVAIG-----YSIG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08657192
                                                                                                                                                                                                                                                                         532 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                              8.0%; Score 80.5; DB 1; Length 532; llarity 30.5%; Pred. No. 2.2; Conservative 15; Mismatches 25; Indels
                                                                                                                                                                                                              linear
                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTANT STAPHYLOCOCCUS AUREUS V8 PROTEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VEMSYEAFDVKNPGDNYKNGAYRYCALSHQDDADDDMTSATDKF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/657,192
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RESULT 10 US-08-523-373-7

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US-08-657-192-3
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                                                                                                                                                                                                                                                                 Sequence 3, Application US/08657192 Patent No. 5747321
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                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
   COMPUTER
MEDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yabuta, Masayuki APPLICANT: Ohsuye, Kazuhiro TITLE OF INVENTION: PROCESS NUMBER OF SEQUENCES: 24
                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                    APPLICANT: YABUTA, Masayuki APPLICANT: OHSUYE, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
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PRIOR APPLICATION DATA;
PRIOR APPLICATION DATA;
DF 6-238595
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MEDIUM TYPE: Floppy disk
                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                         IUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                     289
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Local Similarity 30.58;
nes 18; Conservation
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TOPOLOGY: lir
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STREET: 699 Prince Street
                                                    COUNTRY:
                                                                                    CITY: Alexandria
                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/523,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexandria
                                     ZIP: 22313-1404
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                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                           TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDRLYRRHHRWGR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7, Application US/08523373
5. 6037145
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READABLE FORM:
TYPE: Floppy disk
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                                                                    Virginia
                                                                                                    E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 amino acids
                                                      United States
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                                                                                                                                                                       PROTEASES
                                                                                                                                                                                      MUTANT STAPHYLOCOCCUS AUREUS V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80.5; DB 3; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  001560-251
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                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
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RESULT 12
US-08-523-373-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
                                                      FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: JP 6-2
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
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PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID 176
                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
              REFERENCE/DOCKET NUMBER:
                               REGISTRATION NUMBER:
                                               NAME:
                                                                                                                          APPLICATION NUMBER: JP 6 FILING DATE: 07-SEP-1994
                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 31.5 es 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohsuye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yabuta, Masayuki
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                                                                                                                                                                                                                                                                                                                                                                                              BURNS,
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                                              Donna M.
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                001560-251
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Pred. No.
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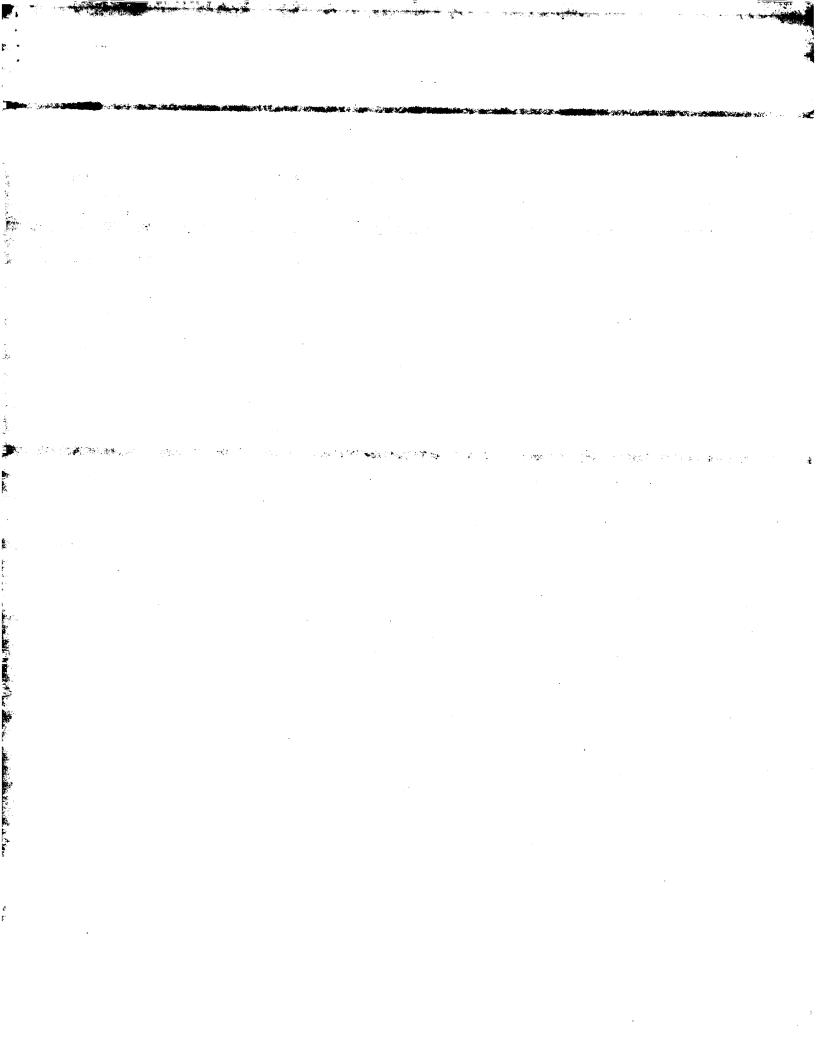
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US-08-523-373-6
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                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: US-08-523-373-6
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                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
ZIP: 22314-318,
ZIP: 22314-318,
COMPUTER READABLE FORM:
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 6-296028 FILING DATE: 07-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 6-238595 FILING DATE: 07-SEP-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
                                                              123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID 176
289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND 342
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/523,373 FILING DATE: 05-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 699 Prince CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Application US/08523373 6037145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meuth, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 Prince Street
                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                      8.0%;
31.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,607
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                                                                                                                                                   13;
                                                                                                                                            Score 80; DB 3; Length 392;
Pred. No. 1.6;
13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    001560-251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Indels
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                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-523-373-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-523-373-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6037145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Apprisequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08523373 Patent No. 6037145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
FILING DATE: 07-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 23317 -- COMPUTER READABLE FORM:
TTVM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-NOV-1994
ATTORNEY AGENT INFORMATION:
NAME: MEULT, DONNA M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION UMBER: JP 6-238595
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHF 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLF 173
                                                                         CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 215 amino acids TYPE: amino acid acid STRANDEDNESS: not relev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-836-2021
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COUNTRY: USA
ZIP: 22314-3187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                  699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-836-6620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 78; DB 3; Length 215; 31.4%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                PROCESS FOR PRODUCTION OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROCESS FOR PRODUCTION OF PROTEIN
                                                                                                                                                                                                                                                             24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC:DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: UF 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION UNMBER: UP 6-238595
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: JF 6-296028
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION UNUMER: 36.607
REFERENCE/DOCKET NUMBER: 36.607
REFERENCE/DOCKET NUMBER: 36.607
REFERENCE/DOCKET NUMBER: 30.566.00
TELECOMMUNICATION INFORMATION:
REGISTRATION UNUMER: 30.660.00
TELECOMMUNICATION INFORMATION:
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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OM protein - protein search, using sw model

Run on: December 20, 2002, 15:49:10; Search time 45 Seconds (without alignments)

.037 Million cell updates/sec

US-10-008-355-2_COPY_522_712

Perfect score: Title:

Scoring table:

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	ø	8	7	6	v	4	ω	2	1		Result No.
79.5		79.5	8	80	80	80	80	80.5	80.5	81	81	81	81.5	81.5	82	82.5	83	84	84	86	86.5	89.5	89.5	89.5	90	93	95	334		Score
7.9			٠	8.0						٠	8.1	8.1	8.1	8.1		8.2		8.4	8.4	. 8.6					9.0				1	Query Match 1
747	389	240	3433	2043	357	342	336	434	325	1104	663	239	603	493	402	759	869	896	729	1060	576	3411	3411	856	711	513	507	716	,	Length 1
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H82943	н86656	C89967	GNWVKV	T18524	S21758	G89873	PRSASK	A29525	E75404	A60999	AG0782	в89967	T04733	G90604	C87291	AE1686	D81832	S46992	AF3591	н86686	в39228	GNWYYP	GNWVY	T13159	S70660	D96980	T34152	G82627		ID
	ന	serine proteinase	genome polyprotein	scavenger receptor		hypothetical prote	glutamyl endopepti	methyl coenzyme M	ABC transporter, A		colicin I receptor	serine proteinase	rt	hypothetical prote	hypothetical prote	pyruvate formate-l	Ĕ.		phat	Ω.	_		genome polyprotein	ElB-55kDa-associat	transferrin-bindin	CO.	_	hypothetical prote		Description

ALIGNMENTS

hypothetical protein XF1887 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-20 C;Accession: G82627

R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, $2000\,$ 20-Aug-2000 #text_change 20-Aug-2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82315; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below A;Accession: G82627
A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-716 <SIM>

A;Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSPDB:GN A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A.Reference number: A59328

A;Contents: annotation C;Genetics: A;Gene: XF1887

5

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Οy	Db	Qy	DЬ	Qy	Db	Qy	Ма	Qu
186 QELKL 190	650 NSGSPVLDAHGKLVGLAFDGNWESVSSNWVFDPVMTRTIAVDSRYVQWIMTEVAPAPHLL 709	126 NSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMIDKWGQCPRLI 185	591 YTPFTTLQGVMAK-NTGVEPFDSPKSLINAIKAKSYANLADQRIGTVPVNFLSDLDITGG 649	68 YNYHTTGKGVLEKODPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGG 125	546 ARPIYLQALAD-YNKSHGKFVYPDANSSLRITFGHVKGYSPKDGVE 590	8 ARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYEPQDGAW 67	Matches 74; Conservative 40; Mismatches 53; Indels 18; Gaps	Query Match 33.3%; Score 334; DB 2; Length 716; Best Local Similarity 40.0%: Pred No. 2.1e-22:

186 OELKL

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В
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                                                                                               Дδ
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A;Title: Genome Sequence and Comparative Analysis of the Solve A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D96980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sensory transduction histidine kinase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D96980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
D96980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Gene: CESP:C33H5.2
A:Introns: 62/2; 109/2; 144/3; 182/2; 208/3; 252/3; 324/3; 370/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F07GI1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Library, November 1995 the company of the sequence of C. elegans cosmid
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                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001437; PIDN:AAK78631.1; PID:915023529; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T34152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Accession: T34
R:Bradshaw, H.;
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                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1~513 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C33H5.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-507 < BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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                     153 GTKNL-KYYSKGQIFIKDLLKNNMSG--KLSIVTDKNDSVIRIQKIDDSVYDKMFGELSN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379
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                                                                                                                                       48
                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 37; Conserv
                                                                                                                                                                                                                                                         CAC0654
                                                         RTKNYGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGL--AFDGNWEAMSGDI-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELNL
                                                                                               FVYEKKGGVIDVYKTEKGRYQNKYTQNYLETIFNNGKVIISTILP--DDYS-EDNLSKCY 152
                                                                                                                                   FTMRMSYGSIKGYEPQDGAWYNYHT-----TGKGVLEKQDPKSDEFAVQENILDLF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSPVFDKNGRLIGLAFDGNWEA---MSGDI-EFEPDLQR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQNANYTWLHYPPVLVNGLEKYEVEENVITHLKTINW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQDPK------SDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIKGKKPLAYFLYHKENYEAFVTPNSSQFSLKNMFGSLK-----CRNFRETGKSVID 333
                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T341
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                                                                                                                                                                           29;
                                                                                                                                                                                           Score 93;
Pred. No.
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Pred. No. 0.84;
                                                                                                                                                                         Mismatches
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                                                                                                                                                                           56;
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                                                                                                                                                                                                             Length 513
                                                                                                                                                                         Indels
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                                                                                                                                                                           28;
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Best Local
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                                       249
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 72
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 TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG-----
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R;Gabler, S.; Schuett, H.; Groitl, P.; Wolf, H.; Shenk, J. Virol. 72, 7960-7971, 1998
A;Title: EIB-55kilodalton-associated protein: A cellular A;Reference number: 217615; MUID:98406198; PMID:9733834
A;Accession: T13159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Homo sapiens (man)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C:Accession: T13159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Microbiol. 19, 159-169, 1996
A;Title: Molecular characterization of hybrid Tbp2 proteins from Neisseria meningitid A;Reference number: S70659; MUID:96419172; PMID:8821945
A;Accession: S70660
                                                                                                                                                                                                                                                         A; Experimental source:
                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-856 < GAB>
                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E1B-55kDa-associated protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;21-711/Product: transferrin-binding protein 2 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent recepto C;Keywords: membrane protein F;1-20/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-711 <L
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C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transferrin-binding protein 2 precursor - Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Legrain, M.; Findeli, A.; Villeval, D.; Quentin-Millet, M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 KNSKSAMQAGESSSQADAKTEQVGQSMFLQG--ERTDEKEIPSEQNIVYR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 SNNDITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV 171
                                                19 AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
                                                                                                   Local Similarity
les 42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PQDGAWYNY---HTTGKG-VLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYE 61
SYGVRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS---YGYG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GSWYGHIASSTSWSGNASDKEGGNRAEFTV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·TAENRQEATFTIDGKIEGNGFSGT--AKTAELGFDLDQKNTTRTPKAYI
                                                                                                   Conservative
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be: HeLa cell line
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                                                                                                                        8.9%; Score 89.5; D
25.1%; Pred. No. 5.2;
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                                                                                                Mismatches
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                                                                                                                                                 Length 856;
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                                                                                                   47;
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F;286-778/Product: major envelope protein E #status predicted <MEE>
F;240-753/Domain: transmembrane #status predicted <TM3>
F;755-778/Domain: transmembrane #status predicted <TM3>
F;755-718/Domain: transmembrane #status predicted <MS1>
F;779-1187/Product: nonstructural protein NS1 #status predicted <NS1>
F;1159-1180/Domain: transmembrane #status predicted <MMS>
F;1159-124/Product: nonstructural protein NS2a #status predicted <N2A>
F;1188-1354/Product: nonstructural protein NS2a #status predicted <N2A>
F;1355-1484/Product: nonstructural protein NS2b #status predicted <N2B>
F;1485-2107/Product: nonstructural protein NS3 #status predicted <NS3>
F;1682-1689/Region: nucleotide-binding motif A (P-loop)
F;1769-1774/Region: nucleotide-binding motif B
F;1773-1776/Region: DEAH motif
                    genome polyprotein - yellow fever virus (strain Pasteur 17D-204)
N;Contains: capsid protein C; envelope protein M; major envelope protein E;
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: yellow fever virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 19-Jan-2001
C;Accession: S07757
C;Accession: S07757
R;Dupuy, A; Despres, P; Cahour, A; Girard, M; Bouloy, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: yellow fever virus genome polyprotein C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; F;2-210/Product: capsid protein C #status predicted <CPC>
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F;2395-2506/Product: nonstructural protein NS4b #status predicted <N4B>
F;2507-3411/Product: nonstructural protein NS5 #status predicted <NS5>
F;2507-3411/Product: nonstructural protein NS5 #status predicted <NS5>
F;134,150,172,266,594,755,908,986,1796,2062,2320,2346,2408,2467,2720,2734,2740/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;249-269/Domain: transmembrane #status predicted <TM1>F;271-285/Domain: transmembrane #status predicted <TM2>
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C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 19-Jan-2001
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    yellow fever virus (strain 17D)

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25.5%;
Cahour,
189, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LFKVRNGG---EIGAVAL----
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Pred. No. 31
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ATYDVKTTGVYAI-KEGTTSQDFAINGVVIGQI---NYKDGDNNGQLVSAINAVKDTTGV

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A;Cross references: EMBE:X15062; NID:g62289; PIDN:CAB37419.1; PID:g4456986
A;Note: the nucleotide sequence was submitted to the EMBE Data Library, April 1989
C;Superfamily: yellow fever virus genome polyprotein
C;Supwords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; 2-210/Product: capsid protein; c **status predicted <CPC>
F;105-125/Domain: transmembrane **status predicted <TM1>
F;211-285/Product: major envelope protein M **status predicted <TM2>
F;286-778/Product: major envelope protein E **status predicted <TM3>
F;36-753/Domain: transmembrane **status predicted <TM3>
F;756-778/Product: nonstructural protein S; **status predicted <NS1>
F;1133-1151/Domain: transmembrane **status predicted <TM5>
F;1133-1151/Domain: transmembrane **status predicted <TM5>
F;1188-1354/Product: nonstructural protein NS2 **status predicted <N2B>
F;135-1484/Product: nonstructural protein NS2*
F;1485-2107/Product: nonstructural protein NS2*
F;169-1794/Region: nucleotide-binding motif A (P-loop)
F;1763-736/Region: DaAH motif
F;210-3304/Product: nonstructural protein NS2*
F;176-3304/Product: nonstructural protein NS2*
F;176-1774/Region: DaAH motif
F;210-3304/Product: nonstructural protein NS2*
F;176-1774/Region: DaAH motif A (P-loop)
F;176-1774/Region: DaAH motif B
F;210-3304/Product: nonstructural protein NS4*
F;2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flagellin B - Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 20-Sep-1991 #sequence_revision
C;Accession: B39228
       QΥ
                                                                                                                                                                                                     A;Cross-references: GB:J05635; NID:g144197; C;Superfamily: flagellin
                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 265, 17798-17804, 1990
A; Title: Structural and functional analysis of two Campylobacter jejuni flagellin gen
A; Reference number: A39228; MUID:91009243; PMID:2211662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Nuijten,
J. Biol. C
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                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-576 < NUI>
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                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                               A; Accession: B39228
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Best Local
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Best Local Similarity
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AWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGG 125
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                                                                                                          Similarity
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yenomic RNA
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                                                                                                      8.6%;
31.5%;
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                                                                                                          Pred.
                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89.5;
Pred. No. 31;
                                                                   core 86.5; Inced. No. 5.9; Mismatches
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                                                                                                                                                                                                                                         PIDN:AAA23025.1; PID:g144199
                                                                                                          .9
                                                                                                                                      DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W.; van
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NSGSPVFDKNGRLIGLAFDGNWEAMSGDI

154

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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella A;Reference number: AD3252; PMID:11756688
A;Accession: AF3591
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C;Superfamily: DNA-directed DNA polymerase III alpha
C;Keywords: nucleotidyltransferase
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                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-729 <KUR>
A; Cross-references: GB: AE008918; PIDN: AAL53897.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           alkaline phosphatase (EC 3.1.3.1) [imported] - Brucella melitensis (strain : C;Species: Brucella melitensis
C;Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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A; Residues: 1-1060 <STO>
A; Cross-references: GB.AE005176; PID:g12723378;
A; Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: H86686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-directed DNA polymerase (EC 2.7.7.7) [imported] - Lactococcus lactis subsp. N;Alternate names: DNA polymerase III, alpha chain 2 C;Species: Lactococcus lactis subsp. lactis
                                                                                                          A; Map position:
                                                                                                                                A; Gene: BMEII0655
                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: AF3591
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                                                                                                                                                                        A; Experimental source: strain 16M
                                                                                                                                                                                                                                                       A; Status: preliminary
  Best Lo
                                                                                    Keywords: phosphoric monoester hydrolase
                                              Query Match
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                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QLVKNRRMTILVEINYIRTHRTKTGQ 931
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  l Similarity
48; Conser
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45; Conservative
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21.7%;
                   8.4%;
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    25;
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Pred. No.
                   Score 84;
Pred. No.
  Mismatches
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13;
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                                                                                                                                                                                            PID:g17984837; GSPDB:GN00191
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58;
                                          Length 729;
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98;
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an, D.; Letes
9;
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transferrin-binding protein B NMA2025 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: D81832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: A novel signaling molecule, p130, A; Reference number: S46992; MUID:94349922; A; Accession: S46992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein pl30 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-ul-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S46992
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  A;Gene: tbpB; |
C;Superfamily:
                                                                          A; Molecule type: DNA
A; Residues: 1-698 < PAR>
A; Cross-references: GB: AL162757;
                                                                                                                                     A; Status: preliminary
                                                                                                                                                         A; Reference number: A81775; A; Accession: D81832
                                                                                                                                                                           A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                R;Parkhill, J.; Achtman, M.; Holroyd, S.; Jagels, K.; L. Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    DЪ
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F; 104-154/Domain: SH3 homology <SH3>
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A; Residues: 1-968 <SAK>
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                                                            A; Experimental source:
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                                          :Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKPDCAAMKTVDLTGIAEIAPEDPEPEFVAFNGKNEIAVTLQENNHIAIVDAASGKILSH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QADAMAN-----AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYEPQD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                  KGQLELQQLKQQERLEQEVSRPI----DHDLANWTPAQPLVP--GRTGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSKDGKLLHESGNTLEHRIARAGHYPEKRNKKGVEIEGAEAAIFGDTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDKNGRLI - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G----AWYNYHTTGKGVLEKQDPK----SDEFAV--QEN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPKFT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENI---- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVACSRAVPEDAKQLASQLHGNASLLFRRTKAPGPGPEGSSSLHLNPTDKASSIQSRPLP 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ILDLFRTKNYGRYAENGQL-
                        NMA2025
    bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SQDSPDGQYENSEGGWMEDYDYVHLQGK----EEQEKTQKELLEKGNIVRQG
                                                          serogroup
pathogen transferrin-binding protein; tonB-dependent recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%;

    James,
Leather,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches
                                                          GB:AL157959; NID:g7380371; PIDN:CAB85244.1; A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 84;
Pred. No.
                                                                                                                                                                                                                                      K.D.; Bentley,
S.; Moule, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GLAFDGNWEAMSGDIEF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forms stable complexes in PMID:8070403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DВ
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                      S.D.; Churcher, C.;
Mungall, K.; Quail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 968,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T.;
                                                                                                                                                                                              Neisseria menigitidis Z2491
                                                                                                                                                                                                                                    K . ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mano, H.; Yazaki, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vivo with v-Crk
                                                                                                                                                                                                                                      Klee,
M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                      S.R.; Mo
Rajandre
                                                                                PID:9738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9,
                                                                                                                                                                                                                                                                                                                                     Z24
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Score

83;

DB

2,

Length

698;

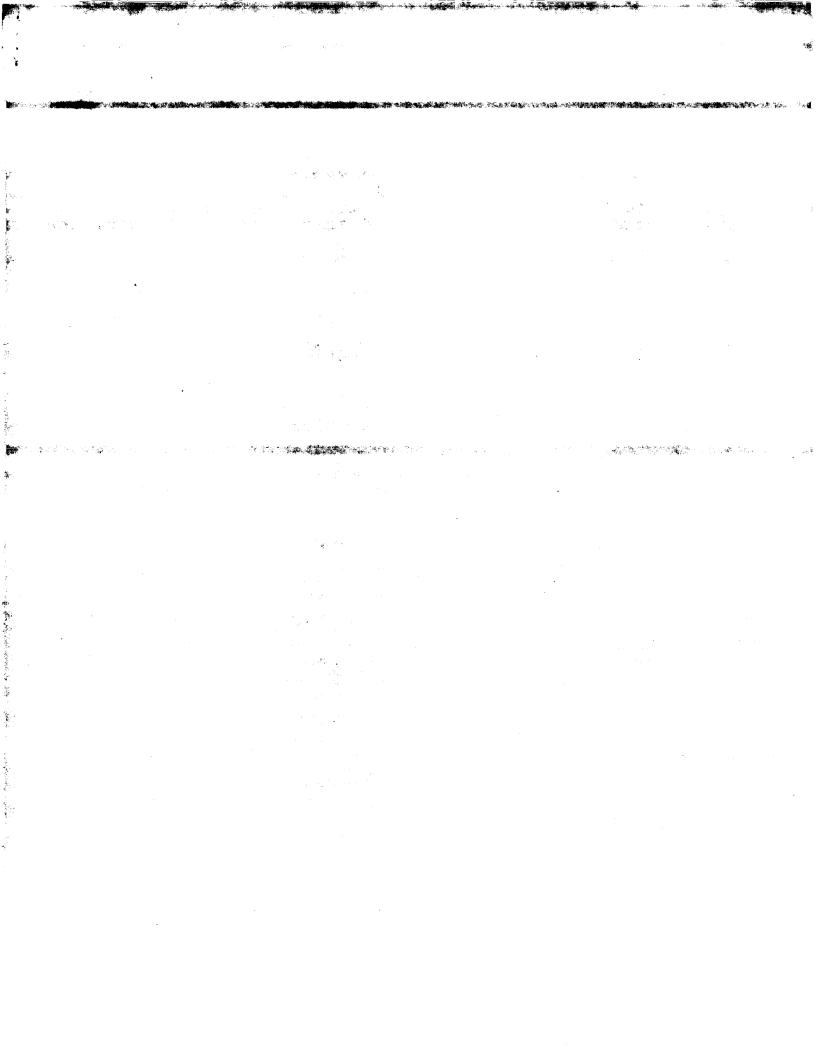
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Дb
                                                                      R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hafn, J.; Ermolaeva, White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-759 <GLA>
A; Cross-references: GB:AL592022; PIDN:C;
A; Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: pflA
C;Superfamily: formate C-acetyltransferase 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Listeria C; Date: 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyruvate formate-lyase homolog pflA [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
A; Status: preliminary A; Molecule type: DNA
                                    A; Reference number: A87249; MUID:21173698; PMID:11259647 A; Accession: C87291
                                                                                                                                                                               hypothetical protéin CC0340 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: AE1686
                                                                                                                                                                   C; Accession: C87291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                          125
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                                                                                                                                                                                                                                                                                                                     611 QCGNSPVHKGPVFDENGKII 630
                                                                                                                                                                                                                                                                                                                                                                                               556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                594 ----TADNRQAATFTIVGDIEGNGFSGT--AKTADSGFDLDQSNNTRTPKAYI 640
                                                                                                                                                                                                                                                                                                                                                                                                                                    73
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                                                                                                                                                                                                                                                                                                                                                                                                                TGK----GVLEKQDPKSDEFAVQENILDLFRTK--NYGRYAEN-GQLHIAFLSNNDITG- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMS---YGSIKGYEPQDGAWYNYHT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTDKYNYESMOMAFLPSKYTANMGFGICGFANVVDSLSAIKYAKVKTIRDEDGFVYDYEV 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUNDITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQDGAWYNYHTTGK----GVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNSKSAMQAGESSSQADAKTEQVGQSMFLQG--ERTDEKEIPNDQNVVYR-----
                                                                                                                                                                                                                                                                                                                                                          --GNS---GSPVFDKNGRLI 139
                                                                                                                                                                                                                                                                                                                                                                                           EGDFPRYG---ENDDRADDIAVM--VLKMFKDKLDSHKLYKDSEATVSVLTITSNVAYSK 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GSWYGHIANGTSWSGNASDKEGGNRADFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #sequence_revision 27-Nov-2001 #text_change 14-Dec-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAC97261.1; PID:g16414532; GSPDB:GN00178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82.5;
Pred. No. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radical homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFGTKKINGTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                           ; Haft,
J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maitournam, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Voss, H.; Wehland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552
                                                                                                         ; Heidelberg, J.
aft, D.H.; Kolon
C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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Fsihi, H.
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Search completed: December 20, Job time: 57 secs

2002,

17:31:37

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RESULT 15
G90604
                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein MYPU_7430 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CC0340
C; Superfamily:
뭥
                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A; Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                          C; Accession: G9: R; Chambaud, I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005673; NID:g13421489; PIDN:AAK22327.1; GSPDB:GN00148 C;Genetics:
                                                                                                                                                                                               A;Cross-references: GB:AL445566; PID:g14090158; PIDN:CAC13916.1; GSPDB:GN00153 A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-493 < KUR>
                                                                                                                                            A; Genetic
                                                                                                                                                               A; Gene: MYPU_7430
                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                         A; Accession: G90604
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
378 KYYYSGLLY--YFRNTALSGGSSGSKTVDKNNKIVGIHALGSDLSGLTGSVAFKSE 431
                               105 RYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGL-AFDGNWEAMSGDIEFEPD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 LQRTISVDIRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 DG---QDVIYKNHYDIGVAVGTDKGLVVPVVRDADALNLAGIEKTIGDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYLALSYDHRIV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGQLAIEDMQGGTFTITNGGIYGSLMSTPILNAPQSGILGMHAIKERPMVINGKIEIRPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGQLHIA-----FLSNNDITGGNSGSPVFD--KNGRLIGLAFDGNWEAMSGDIEFEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAVMALRAQYKDVFEKQHGVKLGFMSFFVKAVVAAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVIAAARAIQADAMANAYAIEKGKRLFF-----AGLREMYPGRALPSDANFTMRMSYGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGYEPQDGAWYNYHTTG-----KGVLEKQDPKSDEF---AVQENILDLFRTKNYGRYAE 108
                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                 G90604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dihydrolipoamide acetyltransferase;
                                                                                                                                            SGC3
                                                                                                                                                                                                                                                                                                                                                            Heilig, R.; Ferris, S.; Barbe, V.;
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
                                                                                      8.1%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 82;
Pred. No.
                                                                                      Pred.
                                                                                    Score 81.5;
Pred. No. 1
                                                                     Mismatches
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                                                                                                     Length 493;
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                                                                   Gaps
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq
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length: 2000000000
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Match
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Gapop 10.0 ,
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 SKSVIAAARAIQADAMANAY.....LFMIDKWGQCPRLIQELKLI 191
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Copyright (c) 1993 - 2002 Compugen Ltd.
 Length
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                                                                                                              BCA1_MOUSE
BCA1_RAT
BCRB_METBA
STSP_STAAU
POLG_KUNJM
APEA_BORBU
CN16_ECOLI
HS7C_TRYBB
YF92_MYCPN
SNTD_VIBPA
CN16_SALTY
ENO_DESVM
RELA_MYCLE
RELA_MYCTU
                                                                                                                                                                  POLG_YEFV2
FLB2_CAMJE
DP3A_LACLA
                                                    EMAP_STRPU
POLG_WNV
TRYE_DROME
                                                                      CLA4_CANAL
POLG_DEN27
                                                                                  BCA1_HUMAN
POLG_JAEVJ
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POLG_DEN2T
                                                                                                                                           TBPB_NEIMA
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TRYE_DROER
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POLG_YEFV1
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P03314 y genome po
P19901 y genome po
P22252 campylobact
     P22848
P26265
O32513
Q49640
                                         Q9prb5
P27914
P12823
P56945
P32886
O14427
Q26613
P06935
P35005
P35005
P35033
                                                                                                                   Q9ci70
Q9sel7
P54627
O68937
Q9tlv0
Q61140
Q63767
P07955
P04188
                             P20030
Q50335
                                                                                                               P14335
                                                                                                                                                                                                     Description
0 trypanosoma
5 mycoplasma
8 vibrio para
5 salmonella
5 salmonella
3 desulfovibr
0 mycobacteri
8 mycobacteri
                                        5 methanosarc
6 stapplococc
6 stapplococc
6 k genome po
5 ureaplasma
4 dengue viru
3 d genome po
6 homo sapien
6 j genome po
7 candida alb
1 d genome po
3 strongyloce
8 w genome po
5 drosophila
5 borrelia bu
1 escherichia
                                                                                                                                          7 arabidopsis
7 drosophila
7 neisseria m
9 bacteriopha
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rattus norv
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Oy Nal	DR DR DR DR SQ SQ SQ Ou	888888888	CCCCE***	R 0 0 0 0 9	G D D D D	RESU YY42 ID		
Best Local Similarity 23.1%; pred. No. 0.31; Matches 37; Conservative 28; Mismatches 45 22 IEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYE	EMBL; U41007; AAA82261.1; WormPep; C33H5.2; CE04146. InterPro; IPR002875; DUF23. Pfam; PF01697; DUF23; 1. ProDom; PD004153; DUF23; 1. ProDom; PD004153; DUF23; 1. Hypothetical protein. SEQUENCE 507 AA; 58572 MW; AFB047FA3SEQUENCE 507 AA; 58572 MW; AFB047FA3SUGUENCE 507 AA; 58572 MW; AA; 58572 AA;	This SWISS-PROT entry is copyright. It is produced through a collabor between the Swiss Institute of Bioinformatics and the EMBL outstat the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comme entities requires a license agreement (See http://www.isb-sib.ch/annoor send an email to license@isb-sib.ch).	SEQUENCE FROM N.A. STRAIN-Bristol N2; Bradshaw H., Stellyes L.; Bradshaw H., Stellyes L.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: BELONGS TO A FAMILY OF C.ELEGANS PROTEIN C27A7.2, C33H5.2, C35A5.5, F13G3.3, F59C6.8, F49C12. AND ZK381.2.	Cael Euk Rhal NCB	DT 15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) DT 15-JUL-1998 (Rel. 36, Last annotation update) DE Hypothetical 58.6 kDa protein C33H5.2 in chromosome IV. GN C33H5.2.	SU 42	ALIGNMENTS	34 75.5 7.5 3391 1 POLG_DEN26 P29990 d genome po 35 75.5 7.5 3391 1 POLG_DEN2N P14340 d genome po 36 75 7.5 3432 1 POLG_JAEV1 P27395] genome po 37 75 7.5 3432 1 POLG_JAEV5 P19110 j genome po 38 74.5 7.4 784 1 OSTA-ECOLI P19110 j genome po 38 74.5 7.4 814 1 CADF_HUMAN P55291 homo sapien 40 74.5 7.4 1254 1 POLS_EEVVB P05674 venezuelan 41 74.5 7.4 1254 1 POLS_EEVVB P36330 venezuelan 42 74.5 7.4 1254 1 POLS_EEVVT P09592 venezuelan 43 74.5 7.4 1255 1 POLS_EEVVP P09592 venezuelan P36329 venezuelan
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RESULT 2

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POLG_YEFV1
ID POLG_YEFV1
AC POSJ314; 042
DT 21-JUL-1986
DE CC 3.4.21.
DE POCTEINS
DE POCTEINS
DE (EC 3.4.21.
DE (NS5)).
OS YELLOW FEVE
OC VITUSES; SE
OC PLAVITUS
RI (NS5).
RA RICE C.M.,
InterPro; IPRO01410; DEAD.
InterPro; IPRO01059; Flavi_MS1.
InterPro; IPRO01157; Flavi_NS1.
InterPro; IPRO00752; Flavi_NS2A.
InterPro; IPRO00752; Flavi_NS2A.
InterPro; IPRO00752; Flavi_NS2A.
InterPro; IPRO00752; Flavi_NS4B.
InterPro; IPRO001528; Flavi_NS4B.
InterPro; IPRO001528; Flavi_NS4B.
InterPro; IPRO00136; Flavi_capsidC.
InterPro; IPRO01850; Flavi_helicase.
InterPro; IPRO01850; Flavi_helicase.
InterPro; IPRO01850; Flavi_propep.
InterPro; IPRO01650; Helicase_C.
InterPro; IPRO01650; Flavi_NS1; 1.
Pfam; PF000949; Flavi_NS1; 1.
Pfam; PF000972; Flavi_NS2B; 1.
Pfam; PF01003; Flavi_NS2B; 1.
Pfam; PF01003; Flavi_NS2B; 1.
Pfam; PF01004; Flavi_NS2A; 1.
Pfam; PF01004; Flavi_NS2A; 1.
Pfam; PF01049; Flavi_NS2A; 1.
Pfam; PF01349; Flavi_NS2A; 1.
Pfam; PF01350; Flavi_NS2A; 1.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix protein (Envelope protein M); Major envelope protein E; Nonstructural proteins NS1, NS2A, NS2B, NS4A and NS4B; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; x03700; CAA27332.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               flavivirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /iruses; ssRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restrictions of the contract of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'. CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate (RNA)(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID PROTEIN C AND MRNA.
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S; S07.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1SVB
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evolution.";
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IS A COMPLEX OF
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POLG_YEFV2 STANDARD; PRT; 3411 AA.

AC P19901;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix
DE protein (Envelope protein M); Major envelope protein E; Nonstructural
DE proteins NS1, NS2B, NS2B, NS4A and NS4B; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
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Best Local
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CARBOHYD
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NP_BIND
SITE
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PROPEP
CHAIN
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Pfam; PF01728; FtsJ; 1.
Pfam; PF02832; Flavi_glycop_C; 1.
ProDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycoprotE; 1.
                                                                                                                                                                                                                             1542
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INIT_MET 1 REMOVED FROM CAPSID PROTEIN CELLULAR AMINOPEPTIDASE.
                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                                                              VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT
                                                                                                                                                                                   AVPGKNVVNVQTKPS---
                                                                                                                                                                                                                                               AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                      -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
                                                                                                                                                                                                                             AFLVRNGKKL.
                                                                                                                                                                                                                                                                    l Similarity
39; Conserv
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211
286
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1159
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                       150
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390
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                                                                                                                                                                                                                                                                                                              MW;
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N-LINKED (GLCNA
                                                                                                                                                                                                                           -IPSWASVKEDLVAYG
                                                                                                                                                                                                                                                                              Score 89.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-DIRECTED RNA POLYMERASE POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
PROTEASE/HELICASE (NS3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPSID PROTEIN
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Helicase;
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pfam; pF01002; Flavi_N;2B; 1.
pfam; pF01003; Flavi_N;2B; 1.
pfam; pF01003; Flavi_N;2A; 1.
pfam; pF01005; Flavi_N;2A; 1.
pfam; pF01349; Flavi_N;4A; 1.
pfam; pF01349; Flavi_N;4A; 1.
pfam; pF01350; Flavi_Diopep; 1.
pfam; pF01728; Flavi_Diopep; 1.
pfam; pF01728; Flavi_N;1; 1.
pfam; pF01283; Flavi_N;1; 1.
pfam; pF01283; Flavi_N;1; 1.
proDom; pD001496; Flavi_N;1; 1.
proDom; pD001496; Flavi_Q1ycoprotE; 1.
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the Euro
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Pfam; PF0(
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Pfam;
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Pfam;
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-I: FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

-I: CATALTYTIC ACTIVITY; Hydrolysis of four peptide bonds in the viprecursor polyprotéin, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

-I: CATALTYTIC ACTIVITY; N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                       Polyprotein; Glycoprotein; Toore protein; Coat protein;
                                                                                                     SMART; SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89282413; PubMéd-2734112;
Dupuy A., Despres P., Cahour A., Girard M.,
"Nucleotide sequence comparison of the geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-89282413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA
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Yellow fever
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exturopean Bioinformatics Institute. There are no restroy non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RNA)(N).
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN M'AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P14336;
                                                                                                                                                                                                                                                                                                                                                   PF00869; Flavi_giycoprot; 1.
PF00948; Flavi_N$1; 1.
PF00949; Flavi_helicase; 1.
PF00972; Flavi_N$5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X15062; CAB37419,1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; IPRO01410; DDAD.
5; IPRO0069; Fiavi_M.
5; IPRO01157; Fiavi_NS1.
6; IPRO01157; Fiavi_NS2A.
6; IPRO00487; Fiavi_NS2B.
6; IPRO01528; Fiavi_NS4B.
6; IPRO01528; Fiavi_NS4B.
6; IPRO01528; Fiavi_NS4B.
7; IPRO01528; Fiavi_NS5B.
7; IPRO01336; Fiavi_ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S07.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long
and this statement is not removed.
requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001850;
IPR002535;
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positivė-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         helicase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flavi_NS2B.
Flavi_NS4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicase_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ft:sJ
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Flavi_helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fiavi_NS2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flavi_propep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fiavi_capsidC
                                                                               Transferase; RNA-directed RNA
                 Envelope protein; Hydrolase;
Nonstructural protein.
REMOVED FROM CAPSID PROTEIN
CELLULAR AMINOPEPTIDASE
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ne P6
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16-OCT-2001
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                                MEDLINE-91009243; PubMed-2211662;
Nuijten P.J., van Asten F.J., Gaastra F
"Structural and functional analysis of
                                                                                                                                                                                                                        1626
                                                                                                                                                                                                                                                                                            1542
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PROPEP
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CHAIN
       "Structural and functional analysis of two Campflagellin genes.";
J. Biol. Chem. 265:17798-17804(1990).
-i- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN
                                                            STRAIN-81116
                                                                                      NCBI_TaxID=197;
                                                                                             Campylobacter.
                                                                                                      Campylobacter jejuni.
Bacteria; Proteobacteria;
                                                                                                                                Flagellin
                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                    SEQUENCE FROM N.A.
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FORM THE FILAMENTS OF BACTERIAL FLAGELLA
                                                                                                                                                                                                                      IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
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                                                                                                                                                                                                                                                                        -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
                                                                                                                                                                                                                                                                                                                                      Similarity
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BY SIMILARITY.
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NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENVELOPE GLYCOPROTEIN M.
MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN, NS2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAPSID PROTEIN
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         POLYMERIZES
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jejuni
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RESULT 5
DP3A_LACLA
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Best Local Similarity
                                                                                                                                                                 MEDLINE-21235186; pubMed-11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
Genome Res. 11:731-753(2001).
FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DP3A_LACLA
Q9CI70;
                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Last sequence update)
DNA polymerase III alpha subunit (EC 2.7.7 2
DNAE OR LL0496.
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INIT_MET
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Interpro; IPR001029; Flagellin_C.
Pfam; PF00669; Flagellin_N; 1.
Pfam; PF00700; Flagellin_C; 1.
PRINTS; PR00207; FLAGELLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J05635; AAA23025.1; -. PIR; B39228; B39228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                              AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY). SUBCELULAR LOCATION: Cytoplasmic (By similarity) SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C SUBFAMILY.
                                                                                         SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THE CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE COLDIMERIZATION TO FORM THE POLITI', COMPLEX. POLITI', ASSOCIATES THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HETEROPOLYMER OF FLAA AND FLAB. SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
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Lactobacillales; Streptococcaceae; Lactococcus
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Pred. No. 2.2;
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2.7.7.7).
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(By similarity).
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                                                                                       DELTA,
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through a collaboration
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                                           STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
MAYOR K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
MAYOR K.F.X., Schueller C., Wambutt R., Entian K.-D., Terryn N.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
Weichselgartner M., Puigdomenech P., Watson M., Schmidtheini T.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Boutry M., Bancroft I.,
                                                                                                                                                                                                                                                                                                                                                                                                                         OSSEL7: 049507;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protease HhoA, Chloroplast precursor (EC 3.4.21.-).
HHOA OR ATAG18370 OR F28J12.30.
Arabidopsis thaliana (Mouse-ear cress).
                 Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T. Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 Lensch M.H.A., Sokolenko A., Herrmann R.G.; "Identification and characterization of the chloroplast HhoA protease, a homolog to the bacterial periplasmic protease HhoA."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryo Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01336; tRNA_anti; 1.
Pfam; PF02231; PHP_N; 1.
SMART; SM00481; POLIIIAC; 1.
TIGRPAMS; TIGR00594; polc; 1
                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Lensch M.H.A., Sokolenko A., Herrmann
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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InterPro; IPR004805;
InterPro; IPR004365;
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 Grymonprez B.,
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21.7%;
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PolC_alpha.
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Pred. No.
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Chuang Y.-J.,
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 Vandenbussche F.,
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RA Dose S., de Haan M., Maarse A., Schaefter M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbold M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Rabee D., Lemcke K., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Prishman D., Haase D., Lemcke K., Mewes H., W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Mattero A., Shah R.,
RA Schuence and Antonoius R., McCombie W.R.,
RA Chen E., Mara M., Martenssen R., McCombie W.R.,
RA Chen E., Mara M., Martenssen R., McCombie W.R.,
                                                    CHAIN
DOMAIN
ACT_SITE
ACT_SITE
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TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The chloroplast lumen from Arabidopsis thaliana.";
Submitted (JUL-2001) to the SWISS-PROT data bank.
-!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
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Bernelser S., Hengel S., Feldpausch M., Lamberth S., Van den Daele H.

Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,

Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.

Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,

Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Kieselbach T.;
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r T., Bothe G., Ramsperger U., Hilbert H.,
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POLY-GLU.

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CHLOROPLAST (POTENTIAL).
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SEQUENCE
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Wang S., Hickey D.A.;

Wang S., Hickey D.A.;

Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xai
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U40653;
HSSP; P00763;
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Drosophila erecta (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Mnscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                PRINTS; PR00722; CHYMOTRYPSIN. SMART; SM00020; Tryp_SPc; 1. PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0015080; Dere\Try-epsilon
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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vrecursor (EC 3.4.21.4).
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    RESULT 8
TBPB_NEIMA
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                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                  Rajandream M.A., Rutherford K.M., Simmonds M., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain
                                                                                                                                                                                                                                                                                                           Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Lavis R.M., Davis R.M., Davis R. Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-22491
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human antibody responses to A and C capsular polysaccharides, protease and transferrin-binding protein complex stimulated by infection with Neisseria meningitidis of subgroup IV-1 or ET-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Z2491 / Serogroup A / Serotype 4A;
Brieske N., Quentin-Millet M.-J., Schenker M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferrin-binding protein 2 precursor TBPB OR TBP2 OR NMA2025.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     068937;
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                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                      anchor (Probable).
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AF058689;
AL162757;
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42; Conserv
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                AAC13725.1;
CAB85244.1;
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23.1%;
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Pred. No. 1.
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RESULT 9
VPS_BPMU
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                             Morgan G., Hatfull G., Hendrix R.;
"Genome of bacteriophage Mu and comparison with the Hae
influenzae Mu-like prophage Flumu.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
-!- SIMILARITY: SOME, TO H.INFLUENZAE HI1522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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InterPro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG
                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S OR 49
                                                                                                                                             Fiber protein
SEQUENCE 50
                                                                                                                                                                      InterPro; IPR005068; Phage_fiber_2.
Pfam; PF03406; Phage_fiber_2; 1.
                                                                                                                                                                                                    EMBL; AF083977; AAF01127.1; -
                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, Mu-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tail fiber protein (gpS).
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                                                                                                                                                             Fiber
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16-OCT-2001 (Rel.
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YEPQDGAWYNYHT - - - - TGKGVLEKQDPKSDEFAVQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNNDITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV 171
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                            ALSVLVNATVNGEVISKSAN----GLRIAYGNYGFFIRNDGSNTYFMLTNSGDNMGTYNG
                                                        ARAIQADAMANAYAIEKGKRLFFAGLREMYP--GRALPSDANFIMRM-----SYGSIKG
                                                                                      46;
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37; Conserv
                                                                                                   Similarity
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21
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75176 MW;
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21.3%;
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19.9%;
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                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83; DB Pred. No. 5.8;
                                                                                                  Score 82; DB Pred. No. 4.8;
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83FBE14DDF617B1F CRC64;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CRK-associated substrate (P130CAS) (Breast cancer anti-estrogen
                                                    MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN CONTAINING A DIVERGENT HELIX-LOOP-HELIX (HLH) MOTIF. THE SH2-BINDING SITES PUTATIVELY BIND CKK, NCK AND ABL SH2 DOMAINS. THE HILH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL.

-! DOMAIN: A SERING-RICH REGION PROMOTES ACTIVATION OF THE SERUM RESPONSE ELEMENT (SRE) (BY SIMILARITY).

-! DOMAIN: THE SH3 DOMAIN IS NECESSARY FOR THE LOCALIZATION OF THE PROTEIN TO FOCAL ADHESIONS AND INTERACTS WITH ONE PROLINE-RICH PROTEIN TO FOCAL ADHESION KINASE 1.

-! PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE YDYVHL MOTIF. THE SRC FAMILY KINASES ARE RECRUITED TO THE PROSPHORYLATED SITES AND CAN PHOSPHORYLATE TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                             <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (IS FOCAL ADHESION KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance 1 protein).
BCAR1 OR CRKAS OR CAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCA1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Donaldson J.C., Dempsey P.J., Reddy S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20249316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase substrate p130Cas.";
Proc. Natl. Acad. Sci. U.S.A. 92:10678-10682(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96068679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanks S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Crk-associated substrate pl30(Cas) interacts with nephrocystin both proteins localize to cell-cell contacts of polarized epithe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polte T.R., Hanks S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTERACTION WITH NEPHROCYSTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interaction between focal adhesion kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315
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                                                                                                                                                                                                                                                                                                                                                                                 EMBRYOGENESIS.
SUBUNIT: FORMS COMPLEXES IN VIVO WITH FOCAL ADHESION KINASE 1,
ADAPTER PROTEIN CRKL AND LYN KINASE. CAN HETERODIMERIZE WITH C
(BY SIMILARITY). INTERACTS WITH NEPHROCYSTIN AND PTK2B.
SUBCELLULAR LOCATION: FOCAL ADHESIONS. UNPHOSPHORYLATED FORM
LOCALIZES IN THE CYTOPLASM AND CAN MOVE TO THE MEMBRANE UPON
                                                                                                                                                                                                                                                                                                                             TYROSINE PHOSPHORYLATION (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAS-B (SHOWN HERE) AND CAS-A;
ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION:
                                                                                                                                                                                                                                                                                                             DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Res. 256:168-178(2000).

FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL COORDINATING FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL COORDINATING FOR TYROSINE-KINASE-BASED SIGNALING RELATED TO CELL ADHESION. IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY). HISEN SHOWN TO BE ESSENTIAL IN CARDIOVASCULAR DEVELOPMENT DURI
RESIDUES. TYROSINE PHOSPHOR MEDIATED ADHESION OF CELLS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYANFDSRYVRDVRLGTQSLTGGLSRDYKAPSGHVITGFHTNGDWEMQGGD 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LWINNATGAVSMGRGLNVSGDTLSDRFAINSSNGMWIQMRDNNAIFGKNIVNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A. (ISOFORMS CAS-A AND CAS-B), AND INTERACTION WITH
                                      TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10739664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                      TO THE EXTRACELLULAR MATRIX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Crk-associated tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epithelial
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RESULT 11
BCA1_RAT
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                                                                                                                                                                                                           BCA1_RAT STANDARD: PRT: 968 AA. Q63766; Q63766; Q63766; 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
       Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Mano H., Yazaki Y., Hirai H.; Yazaki Y., Hirai H.; "A novel signaling molecule, p130, forms stable complexes in vivo v-Crk and v-Src in a tyrosine phosphorylation-dependent manner."; EMBO J. 13:3748-3756(1994).
EMBO
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                               MEDLINE=94349922; PubMed=8070403;
                                                                                                                                                                                              BCAR1 OR CRKAS OR CAS.
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ProDom; PD000066; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                              TISSUE=Fibroblast;
                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00326; SH3; 1.
                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                    Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
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43; Conserv
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AAA93248.1; -.
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                                                                                                            AND
                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                           PARTIAL SEQUENCE
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SUBSTRATE
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Query Match
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EMBL; D29766; 1
HSSP; P07751;
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                                                                                                       SEQUENCE
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J. Biol. Chem. 272:29983-29090(1997).
                                                                                                                                  VARSPLIC
                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tachibana K., Urano
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                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTESTINE AND TESTIS.

INTESTINE AND TESTIS.

DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING MULTIPLE POTENTIAL SH2-SHADING SITES AND A C-TERMINAL DOMAIN CONTAINING A DIVERGENT HELLX-LOOP-HELLX (HLH) MOTIF. THE SH2-BINDING SITES PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS. THE BINDING SITES PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS. THE HLH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODINERIZATION WITH CASL. DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM RESPONSE ELEMENT (SRE).

DOMAIN: THE SH3 DOMAIN IS NECESSARY FOR THE LOCALIZATION OF THE PROTEIN TO FOCAL ADHESIONS AND INTERACTS WITH ONE PROLINE-RICH REGION OF FOCAL ADHESION KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 SH3 DOMAIN. SIMILARITY: BELONGS TO THE CAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE MEMBRANE UPON TYROSINE PHOSPHORYLATION.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE)
AND A SHORT ISOFORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL COORDINATING ROLE FOR TYROSINE-KINASE-BASED SIGNALINAXS ABOUT TO CELL ADBESION. IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY). SUBUNIT: FORMS COMPLEXES IN VIVO WITH FOCAL ADBESION KINASE 1, ADAPTER PROTEIN CAKL AND LYN KINASE. CAN HETERODIMENIE WITH CASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTS WITH NEPHROCYSTIN AND PTK2B (BY SIMILARITY).
SUBCELLULAR LOCATION: FOCAL ADHESIONS AND STRESS FIBERS.
UNPHOSPHORYLATED FORM LOCALIZES IN THE CYTOPLASM AND CAN MOVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: APPEARS TO HAVE A CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE YDYVHL MOTIF. THE SRC FAMILY KINASES ARE RECRUITED TO THE PHOSPHORYLATED SITES AND CAN PHOSPHORYLATE OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN MEDIATED ADHESION OF CELLS TO THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN LUNG
  al Similarity
43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001452; SH3.
                                                                                                                                                                          splicing.
97 159
168 181
213 514
520 712
733 741
                                                                                                       896
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAA06169.1;
BAA06170.1;
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                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                      SH3; 1.
                                                                                                                                                                                                                                                                                                                                    SH3 domain;
                                                                                                                                                                                                                                                                                                                                                               SH3;
                                                                                                       104262 MW;
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                       8.1%;
     17;
Score 81; DB Pred. No. 13; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                 SH3-binding;
                                                                                                                            DIVERGENT HELIX-LOOP-HELIX MOTIF MISSING (IN SHORT ISOFORM).
                                                                                                                                                                               SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                            SER-RICH
                                                                                                                                                                                                                                  SUBSTRATE
                                                                                                                                                                                                                                                         PRO-RICH
                                                                                                     E861641BFD68D377 CRC64;
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                       DB
13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION
                                                                                                                                                                                                                                                                                                                                         Cell adhesion;
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  Indels
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  56;
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                                                                                 Matches
                                                                                             Query Match
Best Local
                                                                                                                                                 Methanogenesis; Oxidoreductase INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                          This
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15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P07955;
01-AUG-1988 (Rel.
                                                                                                                                     SEQUENCE
                                                                                                                                                                            InterPro; IPR003179; MCR_beta
Pfam; PF02241; MCR_beta; 1.
Pfam; PF02783; MCR_beta_N; 1.
                                                                                                                                                                                                                                                EMBL; Y00158; CAA68353.1;
                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                   modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 15:4350-4351(1987).
-!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthic ethanesulfonic acid) with 7-mercaptoheptanoylthreonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Fusaro / D
MEDLINE=87231011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanosarcina barkeri.
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                     HSSP; P11560;
                                                                                                                                                                                                                                   PIR; A29525
                                                                                                                                                                                                                                                                                                                    use
                                                                                                                                                                                                                                                                                                                              the European
                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bokranz M., Klein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCRB_METBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the methyl coenzyme M reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               785
 56
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                                                      N
                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Methanogenesis; last step.
SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: CH(3)-S-COM + H-S-HTP = CH(4) + COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW
                                                                                                                                                                                                                                                                                                                                                                                                                 PORPHINOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to methane and an heterodisulfide.
                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIVRQGK----GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL
--SIKGYEPQDGAWYNYHTTGKGVLEKQDPKS-
                                                      KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGR--ALPSDANFTMRMSYG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPG------
                           RSVAVNLAGIQG-ALASGKMGGKGRQILGRGLNYDIVGNADAIAENVKKLVQVDEGDDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTKNYGRYAENGQLHIAFLS------NNDITGGNSGSPVFDKNGRLIGL 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDLF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVACSRAVPEDAKQLASFLHGNASLLFRRTKAPGPGPEGSSSLHLNPTDKASSIQSRPLP 736
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                non-profit
                                                                                                                                     433 AA;
                                                                                                                                                                                                                   0; 1MRO
                                                                                                                                                                                                                                                                                                                             Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / DSM 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQDSPDGQYENSEGGWMEDYDYVHLQGKEEFEK-----TQKELLEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08, Created)
19, Last sequence 41, Last annotations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3502709;
                                                                                                                                     45289 MW; BABFA4A3709361A9 CRC64;
                                                                                                                                                                                                                                                                                        license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           barkeri
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20.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update
                                                                                 34;
                                                                                                                                                                                                                                                                                      agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                    is not removed.
                                                                                           Score 80.5;
Pred. No. 5
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subunit (EC
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                                                                                 74;
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----DEFAVQENILDLFR
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(BUT NOT COVALENTLY)
A YELLOW NICKEL
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                                                                                                         Length 433;
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RESULT 13
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-1987 (Rel. 04, Created)
01-APR-1988 (Rel. 07, Last equence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glutamyl endopeptidase precursor (EC 3.4.21.19)
InterPro; IPR000126; Ser_proteas_V8
InterPro; IPR001254; Ser_protease_T:
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus protease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carmona C., Gray G.L.;
"Nucleotide sequence of the serine protease gene of Staphylococcus aureus, strain VB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P04188;
                                             PIR; A26812; PRSASK. MEROPS; S01.269; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20569178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteinase)
                                                                          EMBL; AF309515;
                                                                                          EMBL; Y00356; CAA68434.1;
                                                                                                                                                                                                                                                                                                                                                                     Drapeau G.R.;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=78212487; PubMed=96922;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 69-280
                                                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice K., Peralta R., Bast D., de Azavedo J., McGavin M.J.; "Description of staphylococcus serine protease (ssp) operon Staphylococcus aureus and nonpolar inactivation of sspA-ence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87316953; PubMed=3306605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      FUNCTION: PREPERENTIALLY CLEAVES PEPTIDE BONDS ON THE CARBOX TERMINAL SIDE OF ASPARTATE AND GLUTAMATE.

CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-xaa, Glu-|-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B.

DATABASE: NAME-Worthington enzyme manual;

WWW-"http://www.worthington-biochem.com/manual/P/STAP.html".
                                                                                                                                                                                                                                                                                                                                         primary structure of staphylococcal protease. J. Biochem. 56:534-544(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAAU
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                                                                                                                                                                                                                                                                                                                                     Biochem. 56:534-544(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peralta R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes;
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                                                                           AAG45843.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11119502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15:6757-6757(1987).
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   Ser_protease_Try
in; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336
                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWGQC
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                                                                                                                                                                                                                                                                                                                      ON THE CARBOXYL-
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MBL outstation -
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                                                                                                                                                    commercial
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RESULT POLG_KUI
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ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                             Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix protein (Envelope protein M); Major envelope protein E; Nonstructural proteins NS1, NS2, NS4A and NS4B; Protease/helicase (EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48) (NS5)]. Kunjin virus (strain MRM61C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLG_KUNJM STANDARD; PRT; 3433 AA. P14335; Q82983; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                definitive proteins ";
                                                                                                                                                                                                                                                                                                            MEDLINE-88089524; pubMed=2826659;
Coia G., Parker M.D., Speight G., Byrne M.E., Wes
"Nucleotide and complete amino acid sequences of
definitive gene order and characteristics of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00839; V8PROTEASE.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                   J. Gen. Virol.
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SIGNAL
                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Flavivirus
                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID
                                                                                                                                                                                        precursor polyprotein, commonly with Asp or Glu in the position, Cys or Thr in Pl and Ser or Ala in Pl'.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diph
                                                                                                                                                                                                                            FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B AR HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCT NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in t
                                                                                                                                                                (RNA)(N).
SUBUNIT: THE VIRION OF THIS VIRUS IS
                                                                                                                           PROTEIN M AND GLYCOPROTEIN E. PROTEIN C AND MRNA.
                                                                                                                                                      LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease; Zymogen; Signal.
1 29 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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69
119
161
237
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1125
229
268
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                                                                                                                                                     ENVELOPE.
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336
119
161
237
237
125
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261
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31.5%;
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MISSING (IN REF. 3).
N -> D (IN REF. 3).
V -> T (IN REF. 3).
D -> N (IN REF. 3).
EFN -> QFD (IN REF. 3).
ENV -> NEVN (IN REF. 3).
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CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 80;
                                                                                                                                       IS VIRUS IS A NUCLEOCAPSID COVERED ENVELOPE CONSISTS OF TWO PROTEINS:
N E. THE NUCLEOCAPSID IS A COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8B138D0C7996AA3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOPEPTIDASE
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                                                           as its content
                                              Usage
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                                                                                                                                                                                                                                                                                                            Westaway E.G.;
of Kunjin virus:
the virus-specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 336;
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                                                                                      collaboration
                                                                                    outstation
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                                                                                                                                         QF
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                                               commercial
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EMBL; D00246;

BAA00176.1;

HSSP; P14336;

GNWVKV 1SVB.

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Best Local S
Matches 43
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pfam; pr00869; Flavi_glycoprot; 1.

pfam; pr00949; Flavi_NSI; 1.

pfam; pr00949; Flavi_Nelicase; 1.

pfam; pr00949; Flavi_NS5; 1.

pfam; pr01002; Flavi_NS2; 1.

pfam; pr01003; Flavi_NS2; 1.

pfam; pr01004; Flavi_NS2; 1.

pfam; pr01005; Flavi_NS2A; 1.

pfam; pr01005; Flavi_NS4B; 1.

pfam; pr01350; Flavi_NS4A; 1.

pfam; pr01350; Flavi_propep; 1.

pfam; pr01282; Flavi_propep; 1.

pfam; pr02832; Flavi_glycop_C; 1.

pfam; pr02832; Flavi_NS1; 1.

pfam; pr02832; Flavi_NS1; 1.

pfam; pr02832; Flavi_Slycop_C; 1.

proDom; pD001496; Flavi_NS1; 1.

proDom; pD001556; Flavi_NS1; 1.
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InterPro; IPR000157; Flavi_NS1.
InterPro; IPR000752; Flavi_NS2A.
InterPro; IPR000487; Flavi_NS2B.
InterPro; IPR000404; Flavi_NS4A.
InterPro; IPR001528; Flavi_NS4B.
InterPro; IPR001208; Flavi_NS4B.
InterPro; IPR001208; Flavi_GapsidC.
InterPro; IPR001122; Flavi_GapsidC.
InterPro; IPR001356; Flavi_GapsidC.
InterPro; IPR001850; Flavi_helicase.
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NP_BIND
SITE
DISULFID
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InterPro; IPR002877; FtsJ.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Core protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyprotein; Glycoprotein; Transferase; RNA-directed RNA
                                  52 MSYGSIKGYEPQDGAWYN-----YHTTGKGVLEKQDPKSDEF--AVQENILDLFRTKNY 103
MTRGLLGSYQAGAGVMVEGVFHTLWHTTKGAALMSGEGRLDPYWGSVKEDRL------CY 1584
                                                                              l Similarity
43; Conserv
                                                                                                                                                                350
364
382
480
595
138
921
966
998
3433
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coat protein;
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1706
1793
320
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21.4%;
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                                                                                                                                                                381363
                                                                                                 .48;
                                                                              28;
                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Envelope protein; Hydrolase;
Nonstructural protein.
REMOVED FROM CAPSID PROTEIN
                                                                                                                                                                               BY SIMILARITY.
                                                                     Pred. No. /v,
8; Mismatches
                                                                                                 Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                   INVOLVED IN FUSION. ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NONSTRUCTURAL PROTEIN NS2B. PROTEASE/HELICASE (NS3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPSID PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELLULAR AMINOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-DIRECTED RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONSTRUCTURAL PROTEIN NS4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE PROTEIN M
                                                                                                                                                            LINKED (GLCNAC. . . )
LINKED (GLCNAC. . . )
LINKED (GLCNAC. . . . )
LINKED (GLCNAC. . . . )
EE4B888A7D040B99 CR
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76;
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                                                                                                                                                                CRC64;
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                                                                                                                                                                                 (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymerase;
Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NS5).
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                                                                           Gaps
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RESULT 15
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Search completed: December Job time: 37 secs
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y030_UREPA
Q9PRB5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Serovar 3;
MEDLINE-20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass
                                                                                                                                                                                                                                                                                                  Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 7 27 POTENTIAL.
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                            EMBL; AE002102; AAF30435.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                urealyticum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glass J.I., I
Cassell G.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=134821;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 407:757-762(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
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                                                        676
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                                                                                                                                                                                               RLFFAGLREMYPGRALPSDA---NFTMRMSYGS-IKGYEPQDGAWYNYHTTGKGVLEKQD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDKNGDVIGLYGNGVIMPNGSYISAIVQGERMDEPVPAGFEPEMLRKKQITVLDLHPGAG 1704
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                                                        SMIIDSNFNLVGIHFASLNSRAYGAPNDSMIGNLFVAQSQDLSGDID
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                                                                                    SPVFDKNGRLIGLAFD----
                                                                                                                                         PKSDEFAVQENILDLFRTK---NYGRYAENGQLHIAFLSN-----NDITGGNSG 128
                                                                                                                                                                      QLFSGG----YPGDVNPNSSAIVSWRGSKSYGSLIQAF----
                                                                                                              -DREIKNESILDYYGPKQINNIDGYQKVGEGYLNKLFNVGTRVITSDEIGDLGSGSSG
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parvum (Ureaplasma urealyticum biotype 1 Firmicutes; Mollicutes; Mycoplasmataceae;
                                                                                                                                                                                                                                                                                   747 AA; 85860 MW;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein UU030.
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40,
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23.4%;
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Last sequence update)
Last annotation updat
              20,
              2002,
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                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                          Score 79.5;
Pred. No. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                     68FFD940C28D02AF CRC64;
                                                                                                                                                                                                                             Mismatches
                                                                                    -GNW-----EAMSGDIE
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                                                                                                                                                                                                                                           13;
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                                                                                                                                                                                                                                                      Length 747;
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ae; Ureaplasma.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.1580 seqs, 206047115 residues
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1003
1 SKSVIAAARAIQADAMANAY.....LEMIDKWGQCPRLIQELKLI 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	æ	7	6	, U 1	4	· w	Ν	ч	Result No.
89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	90	90.5	93	101.5	334	Score
8.9	8.9	8.9	8.9	8.9	8.9	9	8 9	8.9	8.9	8.9	9.0	9.0	9.3	10.1	33.3	Query Match I
3411	3411	341/1	3411	3411	3411	3411	341,1	859	856	856	711	408	513	305	716	Length DB
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Q89278	Q89277	Q89275	ONMA60	TNMA60	Q9YWN2	091857	298803	Q8VDM6	Q9вил2	076022	Q51284	Q96604	Q97LA8	Q8XUP6	Q9PC94	ID
yellow	Q89277 yellow feve	yellow	yellow	Q9ywn1 yellow feve	yellow		~	mus	Q9buj2 homo sapien	076022 homo sapien	Q51284 neisseria m	Q96604 avian infec	Q97la8 clostridium	Q8xup6 ralstonia s	Q9pc94 xylella fas	Description

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Q8Z597	Q9F474	Q53782	Q9KH49	Q9SZT9	Q93Z39	Q98PH9	Q96605	Q8T6J0	Q9LLS0	Q9AB91	Q92A91	030713	Q9EXC4	OM4F6Ö	Q9EXB5	Q8VE75	Q9FBG1	Q8RGN9	Q994B3	Q8YC77	Q9FD07	085183	Q93ZW5	Q8TL57	Q9YRV3	Q9RF25	Q89276
Q8z597 salmonella		Q53782 staphylococ			Q93z39 arabidopsis		Q96605 avian infec			caulobact	-	030713 flavobacter	Q9exc4 neisseria m	Q9jpmO neisseria m	Q9exb5 neisseria m		Q9fbg1 staphylococ	Q8rgn9 fusobacteri	Q994b3 human immun	7		C		Q8t157 methanosarc	w	O	Q89276 yellow feve

ALIGNMENTS

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de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,	aggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,	a H.A. Jr., Pesquero	iveira M.C., de Oliveira R.C	Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,	Mency C.F.M., MIFACCA E.C., MISCHART C.F., MONTEIFO-VITOFELIO C.B.,	E.A.L., Martins E.M.F., Matsukuma A.Y.,	Madeira A.M.B.N., Madeir	.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado	.E., Kuramae E.E., Laigret F.,	Ωı	er M., Goldman G.H., Goldman M.H.S., Gomes S	Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,	A.J.S., Ferreira V.C.A., Ferro J.A.,	Cristofani M., Dias-Neto E., Docena C., El-Dorry	Costa-Neto C	Camargo A.A., Camargo L.E.A., Carraro D.M., Ca	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,	ga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista (Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,	MEDLINE=20365717; PubMed=10910347;	ASC;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=2371;		D)	Xylella fastidiosa.		f1887.	(TrEMBLrel. 21, Last	(TrEMBLrel. 15.	01-OCT-2000 (TrEMBLrel. 15, Created)	94;	Q9PC94 PRELIMINARY; PRT; 716 AA.	ULT 1 C94

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Best Local
                                                             Matches
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Q8XUP6;
Q1.MAR-2002 (TrEMBLrel. 20, Created)
Q1.MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1.JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative serine protease protein (EC 3.4.21.-)
RSC3140 OR RSO0463.
                                                                                                                                                                                                             Siguler P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
EMBL; AL646073; CAD16849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dd Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A. de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.; "The genome sequence of the plant pathogen Xylella fastidiosa.";
                                                                                                                       Hydrolase;
SEQUENCE
                                                                                                                                                     Pfam; PF00089; trypsin; 1. PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                     Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demang
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ralstonia solanacearum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:151-159(2000).
EMBL; AE004008; AAF84693.1;
MEROPS; S46.001; -.
                                                                                                                                                                                                 InterPro; IPR000104; Antifreeze_1
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                               InterPro; IPR001254; Ser_protease_Try
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                             MANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIK------GYEPQD 64
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ITNCHVLRGGKQVWLK------RGNANFGARLQYPDVERDLCQLRVADFHYPPVT 91
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                                                             l Similarity
33; Conser
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                                                                                                                     Complete proteome. 305 AA; 32269 MW;
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                                                           Conservative
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ia; beta subdivision; Ralstonia
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                                                          Score 101.5; DE Pred. No. 0.32; 24; Mismatches
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Pred. No. 5.1e-22;
D; Mismatches 53
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EAF086E2315BBDFC
                                                                                                                       284EC5874BF94327 CRC64;
                                                                                       DB 16;
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                                                           51;
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Tsuhako M.H.,
                                                                                       Length
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Schiex T.,
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RESULT 4
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ID Q966
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Best Local S
Matches 37
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Pfam; PF02518; HATPase_C; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; Hiska; 1.
             Q96604;
01-FEB-1997
01-FEB-1997
01-DEC-2001
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Q97LA8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus
Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence up
01-OUN-2002 (TrEMBLrel. 21, Last annotation
Sensory transduction histidine kinase.
                                                                 Q96604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterium Clostridium acetobutylicum.
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007581; AAK78631.1; ...
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Noelling J., Breton G., Omelchenko M.V., Make
Gibson R., Lee H.M., Dubbis J., Qiu D., Hitti
Tatusov R.L., Sabathe F., Doucette-Stamm L.,
 Nucleocapsid
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPR004358; Bact_sens_pr_C.
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                                                                                                                                   NKGFKMTSGEFEAAVMHVLYRRFIYIIFII
                                                                                                                                                                                     GTKNL-KYYSKGQIFIKDLLKNNMSG--KLSIVTDKNDSVIRIQKIDDSVYDKMFGELSN
                                                                                                                                                                                                                                                                FTMRMSYGSIKGYEPQDGAWYNYHT-----TGKGVLEKQDPKSDEFAVQENILDLF
                                                                                                                                                                                                              RTKNYGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGL--AFDGNWEAMSGDI--
                                                                                                                                                                                                                                        FVYEKKGGVIDVYKTEKGRYQNKYTQNYLETIFNNGKVIISTILP--DDYS-EDNLSKCY
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                                                                                                                                                                                                                                                                                                                                       Complete proteome.
E 513 AA; 59185 MW; A2F61615182423B3 CRC64;
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
             (TrEMBLrel.
                                       (TrEMBLrel.
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                           Conservative
 protein
                                                                                                                                                          EFEPDLQRTISVDIRYVLFMI 175
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                                                                                                                                                                                                                                                                                                      9.3%;
24.7%;
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HIS_KIN_sig.
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             02,
02,
19,
                                                                                                                                                                                                                                                                                           29;
            Last sequence update)
Last annotation updat
                                        Created)
                                                                                                                                                                                                                                                                                         Score 93; DB
Pred. No. 3.9;
29; Mismatches
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Hitti J., Wolf '
m L., Soucaille |
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RESULT 5
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Best Local S
Matches 37
                                             Query Match
Best Local S
Matches 38
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Q51284;
Q1-NOV-1996
                                                                                                     Signal.
SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Transferrin-binding protein 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97124667; PubMed=8955062; Sapats S.I., Ashton F., Wright P. "Novel variation in the N protein virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian infectious bronchitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                           SEQUENCE
                                                                                                                                                            Legrain M., Findeli A., Villeval D., Quentin-Medicular characterization of hybrid transfer from Neisseria meningitidis.";
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ EMBL; Z50731; CAA90598.1;
                                                                                                                                                                                                                                                                     Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                              TBP2
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                                                                                                                                        Pfam; PF01298;
                                                                                                                                                                                                                      STRAIN=BZ163;
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                                                                                                                                                                                                                                                          NCBI_TaxID=487;
                                                                                                                                                     [nterPro;
518
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KNSKSAMQAGESSSQADAKTEQVGQSMFLQG--ERTDEKEIPSEQNIVYR-----
                      KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYE
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                                             l Similarity
38; Conserv
                                                                                                                                     IPR001677; Transferrin_bind
.298; Lipoprotein_5; 1.
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21
711 AA;
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                                             Conservative
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AA; 45426 MW; F
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711 T
77057 MW;
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the N protein of
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                                                         9.0%;
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                                             28;
                                            Score 90; DB
Pred. No. 12;
28; Mismatches
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Pred. No. 4.9;
17; Mismatches
                                                                                         POTENTIAL.
TRANSFERRIN-BINDING PROTEIN
; 9BC8A1671F6991D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             167
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12;
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RESULT 7
Q9BUJ2
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Best Local
                                                                     Q9BUJ2 PRELIMINARY;
Q9BUJ2; Q9UG75;
01-JUN-2001 (TremBLrel. 17, C:
01-JUN-2002 (TremBLrel. 21, L.
01-JUN-2002 (TremBLrel. 21, L.
E1B-55kDa-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O76022 PRELIMINARY;
O76022:
01-NOV-1998 (TrEMBLrel. 0)
01-NOV-1998 (TrEMBLrel. 0)
01-JUN-2002 (TrEMBLrel. 2)
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02037; SAP; 1.
Pfam; PF00622; SPRY; 1.
SMART; SM00513; SAP; 1.
SMART; SM00449; SPRY; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "EIB-55kilodalton-associated protein: binding activity implicated in nucleoc adenovirus and cellular mRNAs.";
J. Virol. 72:7960-7971(1998).
EMBL; AJ0075599; CAA07548.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=98406198; PubMed=9733834;
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SEQUENCE FROM N.A.
                    NCBI_TaxID=9606
                                                     Homo sapiens (Human)
                                                                DKFZP586D0920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabler S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                              AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM----SYGSIKGYEPQDGAWYNYH 71
                                                                                                                                                                                                         -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY
                                                                                                                                                                                                                                                                                                                    1 Similarity
42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003878; SPRY_domain. IPR003877; SPRY_recepto
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                                 Primates;
                                         Chordata;
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2; Mismatches
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                                Craniata; V
Catarrhini;
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                                                                                    sequence update) annotation update)
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                                           Vertebrata;
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                                          Euteleostomi;
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Best Local S
Matches 42
                                                   Matches
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InterPro; IPR003877; SPRY_receptor.
Pfam; PP02037; SAP; 1.
Pfam; PF00622; SPRY; 1.
PRIMTS; PR01217; PRICHEXTENSN.
SMART; SM00513; SAP; 1.
SMART; SM00549; SPRY; 1.
                                                                                                   Pfam; PF02037; SAP; 1.
Pfam; PF00622; SPRY; 1.
SMART; SM00513; SAP; 1.
SMART; SM00449; SPRY; 1.
SEQUENCE 859 AA; 9600
                                                                                                                                                                                                                                                                                                                         Ol-WAR-2002 (TrEMBLrel. 20, Created)
Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to EIB-55 kDa-associated protein 5.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC021506; AAH21506.1; -.
                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1999)
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                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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InterPro; IPR003878; SPRY_domain.
InterPro; IPR003877; SPRY_receptor
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 250
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                        19 AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
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SYGVRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS---YGYG 306
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1 Similarity 25.1%; Pred. No. 17;
42; Conservative 22; Mismatches
                                                   l Similarity
42; Conser
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856 AA; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heubner D., Mewes H.W.,
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                        Chordata; Rodentia;
                                                                                                      96002 MW;
                                                             8.9%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95784 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D., Mewes H.W., Gassenhuber J., Wie to the EMBL/GenBank/DDBJ databases
                                                  Score 89.5; [
Pred. No. 17;
22; Mismatches
                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                      197328B681DF260E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB9768B74A5F474D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                859
                                                                                                                                                                                                                                                                                                                                                                                                ΑA
                                                                            BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                           Length
                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170
                                                                                                                                                                                                                                                                                           Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NDVIGCFADFE 336
                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
Q98803
밁
                                     Qγ
                                                                                                                                                                        В
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                                                                                    Matches
                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98803;
Q98803;
Q1-FEB-1997
                                                                                                                              PROSITE; PS00962; NIBELLE LE PROSITE; NIBELLE LE PR
                                                                                                                                                                                                                                                pfam; pF01778; FtsJ; 1.
pfam; pF00271; helicase_C; 1.
proDom; pD001496; Flavi_NS1; 1.
proDom; pD001556; Flavi_glycoprotE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
1542
                                                                                                                                                                                                                                                                                                                                      Pfam; PF01350; Flavi_NS4A; 1.
Pfam; PF01349; Flavi_NS4B; 1.
Pfam; PF00972; Flavi_NS5; 1.
Pfam; PF01570; Flavi_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Homogenery, ---
and post epidemic period in west Allic. .
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-85-82H IVORY COAST;
Pisano M.R., Tolou H., Nicoli J.;
"Homogeneity of Yellow fever virus strains isolated during
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U54798; AAA99812.1; HSSP; P14336; ISVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yellow fever virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                        19
AFLVRNGKKL----
                                     AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGNDVELSFTKNGKWMGTAFRTQKEALGGQALYPHVLVKNCAVEFNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF02832; Flavi_glycop_C;
PF00949; Flavi_helicase;
PF01004; Flavi_M; 1.
PF00948; Flavi_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR001865; Ribosomal_S2.
PF01003; Flavi_capsid; 1.
PF00869; Flavi_glycoprot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG-----
                                                                                                                                                                                                                                    SM00490; HELICC;
                                                                                  Similarity
39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000487;
IPR000404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000069; Flavi_M.
IPR001157; Flavi_NS1
IPR000752; Flavi_NS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001410; DEAD.
IPR001122; Flavi_capsidC.
IPR000336; Flavi_glycoprotE.
IPR001850; Flavi_helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 (TrEMBLrel.
7 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                             )5; Flavi_NS2A;
)2; Flavi_NS2B;
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Flavi_NS2A.; Flavi_NS2B.; Flavi_NS4A.
                                                                                                    8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flavi_NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavi_NS4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavi_propep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicase_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02,
20,
---IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1585
                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                    Score 89.5; DB 12
Pred. No. 1.1e+02;
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  β
                                                                                                                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NDVIGCFADFE 337
                                                                                  46;
                                                                                  Indels
                                                                                                                     Length
                                                                                                                            3411;
                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidemic
                                                                                Gaps
                                        71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
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RESULT 10
091857
                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
  Query Match
Best Local S
Matches 39
                                                                                       pfam; pF01003; Flavi_capsid; 1.

pfam; pF02832; Flavi_glycoprot; 1.

pfam; pF02832; Flavi_glycop_C; 1.

pfam; pF00949; Flavi_Nelicase; 1.

pfam; pF00949; Flavi_Nelicase; 1.

pfam; pF01004; Flavi_NS2A; 1.

pfam; pF01005; Flavi_NS2A; 1.

pfam; pF01002; Flavi_NS2B; 1.

pfam; pF01350; Flavi_NS4B; 1.

pfam; pF01350; Flavi_NS4B; 1.

pfam; pF01378; Flavi_NS4B; 1.

pfam; pF0178; Flavi_NS5; 1.

pfam; pF0178; Flavi_NS5; 1.

pfam; pF0178; Flavi_NS5; 1.

pfam; pF0178; Flavi_NS1; 1.

pfam; pF0178; FtsJ; 1.

pfam; pF00271; helicase_C; 1.

proDom; pD001496; Flavi_NS1; 1.

proDom; pD001556; Flavi_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998
01-NOV-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        091857
091857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98376360; PubMed=9712515; Xie H., Cass A.R., Barrett A.D.T.; "Yellow fever 17D vaccine virus isolated accumulates very few mutations."; Virus Res. 55:93-99(1998). EMBL; AF052438; AAG35900.1; -. HSSP; P14336; 1SVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1586
                                                ATP-binding; Helicase. SEQUENCE 3411 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=17D-204-USA VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yellow fever virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyprotein.
                                                                       PROSITE;
                                                                                     SMART; SM00490;
                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11089;
                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVPGKNVVNVQTKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
   39;
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S07.001
                                                                       PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                       IPR000069;
IPR001157;
IPR000752;
                                                                                                                                                                                                                                                                                                     IPR002877;
IPR001650;
                                                                                                                                                                                                                                                                                          IPR001865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (TrEMBLrel.
3 (TrEMBLrel.
2 (TrEMBLrel.
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                  HELIC¢;
                                                                                                                                                                                                                                                                                                                                                                                                                        Flavi_glycoprotE.
Flavi_helicase
            25.5%;
                                                                                                                                                                                                                                                                                      Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                        Flavi_NS4B.
Flavi_NS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavi_capsidC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAD
                                                                                                                                                                                                                                                                                                                         Flavi_propep
                                                                                                                                                                                                                                                                                                                                                              Flavi_NS4A.
                                                                                                                                                                                                                                                                                                                                                                           Flavi_NS2A.
Flavi_NS2B.
                                                                                                                                                                                                                                                                                                                                                                                                  Flavi_NS1.
                                                                                                                                                                                                                                                                                                                                                                                                            Flavi_M.
                                               379584
                                                                                                                                                                                                                                                                                                    Felicase_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08,
20,
                                                MW;
Score 89.5; D
Pred. No. 1.1e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LFKVRNGG---EIGAVAL-----DYPSGTSGSP 1625
                                                DBF07B82E9F6035C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
             .1e+02
                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from healthy vaccinees
  46;
                      Length 3411;
                                                CRC64;
  Indels
 47;
 Gaps
 8
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RESULT
Q9YWN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
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    В
                                                                   Pfam; PF01003; Flavi_capsid; 1.

Pfam; PF01003; Flavi_glycoprot; 1.

Pfam; PF02832; Flavi_glycoprot; 1.

Pfam; PF02832; Flavi_glycopcC; 1.

Pfam; PF00949; Flavi_Melicase; 1.

Pfam; PF01004; Flavi_MS1; 1.

Pfam; PF01005; Flavi_MS2A; 1.

Pfam; PF01005; Flavi_MS2A; 1.

Pfam; PF01350; Flavi_MS2B; 1.

Pfam; PF01349; Flavi_MS4B; 1.

Pfam; PF01379; Flavi_MS4B; 1.

Pfam; PF01379; Flavi_MS5; 1.

Pfam; PF01778; Flavi_MS6; 1.

Pfam; PF01778; FtsJ; 1.

Pfam; PF01778; FtsJ; 1.

Pfam; PF01778; FtsJ; 1.
PROSITE; PSOUPOL,
ATP-binding; Heli
ATP-DINGE 3411/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9YWN2;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                              Pfam; PF00271; helicase_C; 1.
ProDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-17D-204-SOUTH AFRICA VACCINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyprotein.
Yellow fever virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1542
                                      SMART; SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF052444; AAC35906.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 fever 17D vaccine virus.";
J. Gen. Virol. 79:1895-1899(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xie H., Ryman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flavivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9YWN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1626 IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1586
                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S07
                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P14336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98378039; PubMed=9714237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutation in NS5 protein attenuates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVPGKNVVNVQTKPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
                         PS00962; RIBOSOMAL_S2_1;
                                                                                                                                                                                                                                                                                                                     IPR000752;
                                                                                                                                                                                                                                      IPR001865;
                                                                                                                                                                                                                                                                                                                                                                                          IPR001410;
IPR001122;
                                                                                                                                                                                                                                                                                               IPR001528;
                                                                                                                                                                                                                                                                                                           IPR000404;
                                                                                                                                                                                                                                                                                                                                                                   IPR000336;
IPR001850;
                                                                                                                                                                                                                                                  IPR001650;
                                                                                                                                                                                                                                                             IPR002877;
                                                                                                                                                                                                                                                                                    IPR000208,
                                                                                                                                                                                                                                                                                                                                             IPR001157;
                                                                                                                                                                                                                                                                                                                                                         IPR000069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
               Helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                            1SVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.D., Campbell G.A.,
                                            Flavi_glycoprotE;
                                                                                                                                                                                                                                                                                                        Flavi_NS2A.
Flavi_NS2B.
Flavi_NS4A.
                                                                                                                                                                                                                                                                                 Flavi_NS4B.
Flavi_NS5.
                                                                                                                                                                                                                                  Helicase_C.
Ribosomal_S2.
                                                                                                                                                                                                                                                                    Flavi_propep.
                                                                                                                                                                                                                                                                                                                                                        Flavi_M
                                                                                                                                                                                                                                                                                                                                                                   Flavi_glycoprotE.
Flavi_helicase.
                                                                                                                                                                                                                                                                                                                                          Flavi_NS1.
                                                                                                                                                                                                                                                                                                                                                                                           Flavi_capsidC.
   379510 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IPSWASVKEDLVAYG----GSWKLEGRWDGEEEVQLIA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation updat
   8AAC0F24F65DC50C CRC64;
                         UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrett A.D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse neurovirulence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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Query Match

8.98;

Score 89.5;

DB 12;

Length 3411;

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PRESULT OF THE PRESUL
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Matches
                                  Interpro; IPRO01865; Ribosomal_S2.

Pfam; PF00869; Flavi_glycop_C; 1.

Pfam; PF00869; Flavi_glycop_C; 1.

Pfam; PF00949; Flavi_helicase; 1.

Pfam; PF01004; Flavi_M; 1

Pfam; PF01004; Flavi_NS1; 1.

Pfam; PF01005; Flavi_NS2B; 1.

Pfam; PF01005; Flavi_NS2B; 1.

Pfam; PF01005; Flavi_NS2B; 1.

Pfam; PF01350; Flavi_NS4B; 1.

Pfam; PF01349; Flavi_NS4B; 1.

Pfam; PF01379; Flavi_NS5; 1.

Pfam; PF00972; Flavi_NS5; 1.

Pfam; PF00271; helicase_C; 1.

ProDom; PD001496; Flavi_NS1; 1.

ProDom; PD001496; Flavi_NS1; 1.

ProDom; PD001556; Flavi_NS1; 1.

ProDom; PD001556; Flavi_NS1; 1.

ProDom; PD001556; Flavi_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9YWN1
O9YWN1;
O1-MAY-1999 (TrEMBLrel. 1
O1-MAY-1999 (TrEMBLrel. 1
O1-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
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InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF052445;
HSSP; P14336; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mutation in NS5 protein attenuate: fever 17D vaccine virus.";
J. Gen. Virol. 79:1895-1899(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=17D-204-SOUTH AFRICA VACCINE;
MEDLINE=98378039; PubMed=9714237;
Xie H., Ryman K.D., Campbell G.A., Barrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPGKNVVNVQTKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFLVRNGKKL-----IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
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                          SM00490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fever virus
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39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o; IPR001122; Flavi_capsidC.
o; IPR000336; Flavi_hlycoprotE.
o; IPR001850; Flavi_helicase.
o; IPR00169; Flavi_M.
o; IPR001157; Flavi_NS1.
o; IPR0004752; Flavi_NS2A.
o; IPR0004752; Flavi_NS2B.
o; IPR000404; Flavi_NS4B.
o; IPR001528; Flavi_NS4B.
o; IPR001528; Flavi_NS4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S07.001;
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                        HELICe;
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HELIX_LOOP_HELIX; UNKNOWN_1.
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Flavi_NS4B.
Flavi_NS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flavi_propep
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20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attenuates mouse neurovirulence
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Last annotation update)
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1; Mismatches 46;
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RESULT
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9YWNO;
Q9YWNO;
01-MAY-1999
01-MAY-1999
01-MAR-2002
                                                                                                   Pfam;
                                                                                                                              InterPro;
InterPro;
                                                                                                                                                 InterPro;
InterPro;
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InterPro;
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                                    Pfam;
Pfam;
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Pfam;
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Pfam;
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                                                                                                                                                                                                                                                                                                                     STRAIN=17D-204-SOUTH AFRICA VACCINE;
MEDLINE=98378039; pubMed=9714237;
Xie H., Ryman K.D., Campbell G.A., Barrett A.D.T.;
"Mutation in NS5 protein attenuates mouse neurovir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1. ATP-binding; Helicase. SEQUENCE 3411 AA; 379556 MW; 1AA3ED79510
                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                    InterPro;
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                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                          MEROPS;
                                                                                                                                                                                                                                                                                                             fever 17D vaccine virus."
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11089;
                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                        Yellow fever virus
                                                                                                                                                                                                                                                                                                                                                                                                                  Polyprotein
                                                                                                                                                                                                                                                                                    HSSP;
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                                                                                                                                                                                                                                                                                                      Gen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVPGKNVVNVQTKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP
                                                                                                                                                                                                                                                                                    P14336;
                                                                                                                                                                                                                                                                                             AF052446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Similarity 25.5
39; Conservative
                                                                                                                                                                                                                                                                          S07
                                                                                                                                                                                                                                                                                                    Virol. 79:1895-1899(1998).
                                                                                                                                                                                                        IPR000069;
IPR001157;
IPR000752;
                                                                                                                                                                                      IPR000487;
IPR000404;
                                                                                                                                IPR001865;
                                                                                                                                         IPR001650;
                                                                                                                                                             IPR002535;
                                                                                                                                                                              IPR001528;
                                                                                                                                                                                                                                    IPR001850;
                                                                                                                                                                                                                                                                 IPR001410;
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) (TrEMBLrel.
) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                   1SVB
                          Flavi_NS4A;
Flavi_NS4B;
Flavi_NS5; 1
                                                                                                    Flavi_glycoprot; 1.
Flavi_glycop_C; 1.
                                                                       Flavi_NS1;
                                                                                           Flavi_helicase;
                                                                                                                       Flavi_capsid; 1.
helicase_C;
               Flavi_propep;
                                                      Flavi_NS2A;
Flavi_NS2B;
                                                                                  Flavi_M;
                                                                                                                                                                                                                                                                                            AAC35908.1;
                                                                                                                                                                                                                                 ; DEAD.
; Flavi_capsidC.
; Flavi_glycoprotE.
; Flavi_helicase.
                                                                                                                                                                  Flavi_M.
Flavi_NS1.
Flavi_NS2A.
Flavi_NS2B.
Flavi_NS4B.
Flavi_NS4B.
Flavi_NS4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%;
25.5%;
                                                                                                                              Ribosomal_S2
                                                                                                                                                         Flavi_propep
                                                                                                                                         Helicase_C
                                                                                                                                                                                                                                                                                                                                                                                                                            10,
10,
20,
                                   PPPP
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Last sequence
Last anno
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Pred. No. 1.1e+02
1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1AA3ED795108EABC
                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update) annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                               no DNA stagė;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                        neurovirulence
                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                               Flaviviridae;
                                                                                                                                                                                                                                                                                                                        of yellow
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O89275; PRELIMINARY;
O89275; O1-NOV-1996 (TrEMBLrel, O1,
O1-DEC-2001 (TrEMBLrel, 19,
O1-JUN-2002 (TrEMBLrel, 21,
                                                                                                            InterPro;
InterPro;
                          Pfam;
Pfam;
                                                   Pfam;
Pfam;
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SEQUENCE 3411 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycoprotE; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                        EMBL; U17066; AAC54267.1; -. HSSP; P14336; 1SVB.
                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                        STRAIN=VACCINE STRAIN 17DD;
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VACCINE STRAIN 17DD;
MEDLINE=95274286; PubMed=7754673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yellow fever virus
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                                                                          InterPro;
                                                                                    InterPro;
                                                                                                  InterPro;
                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                       17DD
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11089;
                                                                                                                                    InterPro;
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                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                Complete nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
irPro; IPR001650; Helicase_C.
irPro; IPR001665; Ribosomal_S2.
n; PF01003; Flavi_cabsid; 2.
n; PF00869; Flavi_glycoprot; 2.
n; PF02832; Flavi_glycop_C; 2.
n; PF00949; Flavi_helicase; 2.
n; PF01004; Flavi_M; 2.
n; PF010048; Flavi_NS1; 2.
                                                                                                                                                                                                                                                                                                                                                                                        Santos C.N., Post P.R., Carvalho R., Ferreira I.I.,
                                                                                                                                                                                                                                                                                                                                                       and 17D-213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPGKNVVNVQTKPS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFLVRNGKKL------IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                 J: IPRO01850; Flavi_helicase.
J: IPRO01659; Flavi_M.
J: IPRO01157; Flavi_NS1.
J: IPRO01752; Flavi_NS2A.
J: IPRO00487; Flavi_NS2B.
J: IPRO004487; Flavi_NS4B.
J: IPRO01528; Flavi_NS4B.
J: IPRO01528; Flavi_NS4B.
                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                   IPR001122; Flavi_capsidC.
IPR000336; Flavi_glycoprotE.
                                                                                                        IPR000208; Flavi_NS5.
IPR002535; Flavi_propep.
                                                                                                                                                                                                                                                                             (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                  IPR002877; FtsJ.
                                                                                                                                                                                                                                              IPR001410; DEAD
                                                                                                                                                                                                                                                                                                                                         35:35-41(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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Pred. No. 1.1e
?1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 of yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LFKVRNGG---EIGAVAL-----DYPSGTSGSP 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8A9B127F6623A933
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                                                                                                                                                                                                                                                                                                                                                                 fever virus
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                                                                                                                                                                                                                                                                                                                                                                 vaccine strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
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RESULT 15
Q89277
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Best Local
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Pfam; PF01302; Flavi_NS4B; 2.
Pfam; PF01350; Flavi_NS4B; 2.
Pfam; PF01349; Flavi_NS4B; 2.
Pfam; PF01349; Flavi_NS5; 2.
Pfam; PF01570; Flavi_Propep; 2.
Pfam; PF0172B; Ftsy; 2.
Pfam; PF0172B; Ftsy; 2.
Pfam; PF00271; helicase_C; 2.
ProDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycoprotE; 1
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ATP-binding; Helicase.
CHAIN 211 285
CHAIN 211 285
CHAIN 779 1187
CHAIN 1188 1354
CHAIN 1188 1354
CHAIN 1355 1483
CHAIN 1484 2106
CHAIN 2108 2394
CHAIN 2395 2506
CHAIN 2507 2507
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Q89277;
Q1-NOV-1996
Q1-DEC-2001
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SEQUENCE
                                                                               strain of yellow fever virus with neurotropic vaccine.";
J. Gen. Virol. 76:2749-2755(1995).
                                                                                                             SEQUENCE FROM N.A.
STRAIN-FRENCH NEUROTROPIC VIRUS;
MEDLINE-96068808; PubMed-7595382;
Wang E., Ryman K.D., Jennings A.D.,
Sanders P.G., Barrett A.D.;
"Comparison of the genomes of the w:
                                                                                                                                                                                                                                                                                                                                                                                                                            1542
        Submitted (FEB-1995) to the EMBL; U21055; AAA99712.1; - HSSP; P14336; 1SVB.
                                      Wang
                                                                                                                                                                                                                                                                                                                                                                                   1586
                                                                                                                                                                                                  Flavivirus
                                                                                                                                                                                                            Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                            01-JUN-2002
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SMART; SM00490; HELICC;
                                                  STRAIN-FRENCH
                                                           SEQUENCE FROM
                                                                                                                                                                                       NCBI_TaxID=11089;
                                                                                                                                                                                                                       Yellow fever virus
                                                                                                                                                                                                                                Polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 25.9
39; Conservative
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IPR001410; DEAD
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286
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2507
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                                                N.A.
NEUROTROPIC VIRUS;
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21,
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                             EMBL/GenBank/DDBJ
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Last annotation updat
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Pred. No. 1.1e-
21; Mismatches
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POTENTIAL.
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                                                                                                               wild-type
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                                                                                                                                   Wood D.J.,
                                                                                                      vaccine
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                             databases
                                                                                                      derivative
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                                                                                                                                    Taffs
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Search completed: December 20, Job time: 104 secs
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Best Local S
Matches 39
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InterPro; IPR00135; Flavi_dlycoprotE.
InterPro; IPR00136; Flavi_M.
InterPro; IPR001065; Flavi_M.
InterPro; IPR001057; Flavi_NS1.
InterPro; IPR001057; Flavi_NS2A.
InterPro; IPR000404; Flavi_NS2A.
InterPro; IPR000404; Flavi_NS2A.
InterPro; IPR0001528; Flavi_NS2A.
InterPro; IPR001528; Flavi_NS2A.
InterPro; IPR0020535; Flavi_NS2A.
InterPro; IPR002535; Flavi_NS2A.
InterPro; IPR001655; Helicase_C.
InterPro; IPR001657; Helicase_C.
InterPro; IPR001657; Helicase_C.
InterPro; IPR00185; Ribosomal_S2.
Pfam; PF000869; Flavi_dlycoprot; 2.
Pfam; PF00948; Flavi_dlycop.C; 2.
Pfam; PF00948; Flavi_MS2A; 2.
Pfam; PF01002; Flavi_NS2A; 2.
Pfam; PF01002; Flavi_NS2B; 2.
Pfam; PF01002; Flavi_NS2B; 2.
Pfam; PF010350; Flavi_NS2B; 2.
Pfam; PF010728; Flavi_NS5; 2.
Pfam; PF00971728; Flavi_NS5; 2.
Pfam; PF007728; Flavi_NS5; 2.
Pfam; PF007728; Flavi_NS5; 1.
PF0DDOM; PD001496; Flavi_NS1; 1.
PF0DDOM; PD001556; Flavi_NS1; 1.
PF0DOM; PD001556; PD00
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CHAIN
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                                                                                                                                                                                                                                                1542
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                                                                                                                                                              1586 AVPGKNVVNVQTKPS------LFKVRNGG---EIGAVAL-----DYPSGTSGSP 1625
                                                                                                                         131 VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
                                                                                                                                                                                   72 -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
                                                                                                                                                                                                                                                                               19 AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                                                                                                                                         / Match 8.9%; Score 89.5; DB 12; Length 3411;
Local Similarity 25.5%; Pred. No. 1.1e+02;
nes 39; Conservative 21; Mismatches 46; Indels 47;
                                                                                 : ::|| :||| :| : || | : :|
IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
                                                                                                                                                                                                                                            AFLVRNGKKL-----IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00962; RIBOSOMAL_S2_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                    211
286
779 1
1188 1:
1355 1:
1484 2:
2108 2:
2395 2:5
2507 34
                                                                                                                                                                                                                                                                                                                                                                                                                         ; Helicase.

2 121

211 285

216 778

779 1187

1188 1354

355 1483

484 2106

108 2394

395 2506

107 3411
                                                                                                                                                                                                                                                                                                                                                                                                        379183 MW; E7A5E79C999C9D8D CRC64;
                    2002, 17:30:35
                                                                                                                                                                                                                                                                                                                                                                                                                             NS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NS1.
NS2A.
NS2B.
NS3.
NS4A.
NS4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAPSID PROTEIN C. M PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENVELOPE PROTEIN E.
                                                                                                                                                                                                                                                                                                                           Indels 47;
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                   71
                                                                                                                                                                                                                                                                                                                           8
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